



## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Reed, Steven G.  
Skeiky, Yasir  
Dillon, Davin C.  
Campos-Neto, Antonio
- (ii) TITLE OF INVENTION: Compounds and Methods for  
Immunotherapy and Diagnosis of Tuberculosis
- (iii) NUMBER OF SEQUENCES: 155
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Townsend and Townsend and Crew LLP
  - (B) STREET: Two Embarcadero Center, Eighth Floor
  - (C) CITY: San Francisco
  - (D) STATE: California
  - (E) COUNTRY: USA
  - (F) ZIP: 94111-3834
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 09/724,685
  - (B) FILING DATE: 28-NOV-2000
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/523,436
  - (B) FILING DATE: 01-SEP-1995
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/533,634
  - (B) FILING DATE: 22-SEP-1995
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/620,874
  - (B) FILING DATE: 22-MAR-1996
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/659,683
  - (B) FILING DATE: 05-JUN-1996
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/680,574
  - (B) FILING DATE: 12-JUL-1996
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: WO PCT/US96/14674
  - (B) FILING DATE: 30-AUG-1996
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/730,511
  - (B) FILING DATE: 11-OCT-1996

## (vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/818,112
- (B) FILING DATE: 13-MAR-1997

## (viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Bastian, Kevin L.
- (B) REGISTRATION NUMBER: 34,774
- (C) REFERENCE/DOCKET NUMBER: 014058-008561US

## (ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (415) 576-0200
- (B) TELEFAX: (415) 576-0300

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 766 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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CGAGGCACCG GTAGTTTGAA CCAAACGCAC AATCGACGGG CAAACGAACG GAAGAACACA      60
ACCATGAAGA TGGTGAAATC GATCGCCGCA GGTCTGACCG CCGCGGCTGC AATCGGCGCC      120
GCTGCGGCCG GTGTGACTTC GATCATGGCT GGCGGCCCGG TCGTATACCA GATGCAGCCG      180
GTCGTCTTCG GCGCGCCACT GCCGTTGGAC CCGGCATCCG CCCCTGACGT CCCGACCGCC      240
GCCCAGTTGA CCAGCCTGCT CAACAGCCTC GCCGATCCCA ACGTGTCTGT TGCGAACAAG      300
GGCAGTCTGG TCGAGGGCGG CATCGGGGGC ACCGAGGCGC GCATCGCCGA CCACAAGCTG      360
AAGAAGGCCG CCGAGCACGG GGATCTGCCG CTGTCTGTTCA GCGTGACGAA CATCCAGCCG      420
GCGGCCGCCG GTTCGGCCAC CGCCGACGTT TCCGTCTCGG GTCCGAAGCT CTCGTGCGCG      480
GTCACGCAGA ACGTCACGTT CGTGAATCAA GGCGGCTGGA TGCTGTCACG CGCATCGGCG      540
ATGGAGTTGC TGCAGGCCGC AGGGNAACTG ATTGGCGGGC CGGNTTCAGC CCGCTGTTCA      600
GCTACGCCGC CCGCCTGGTG ACGCGTCCAT GTCGAACACT CGCGCGTGTA GCACGGTGCG      660
GTNTGCGCAG GGNCGCACGC ACCGCCCGGT GCAAGCCGTC CTCGAGATAG GTGGTGNCTC      720
GNCACCAGNG ANCACCCCN NNTCGNCNNT TCTCGNTGNT GNATGA                      766

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## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGCATCACC ATCACCATCA CGATGAAGTC ACGGTAGAGA CGACCTCCGT CTTCCGCGCA	60
GACTTCCTCA GCGAGCTGGA CGCTCCTGCG CAAGCGGGTA CGGAGAGCGC GGTCTCCGGG	120
GTGGAAGGGC TCCCGCCGGG CTCGGCGTTG CTGGTAGTCA AACGAGGCCC CAACGCCGGG	180
TCCCGGTTCC TACTCGACCA AGCCATCACG TCGGCTGGTC GGCATCCCGA CAGCGACATA	240
TTTCTCGACG ACGTGACCGT GAGCCGTCGC CATGCTGAAT TCCGGTTGGA AAACAACGAA	300
TTCAATGTCT TCGATGTCGG GAGTCTCAAC GGCACCTACG TCAACCGCGA GCCCGTGGAT	360
TCGGCGGTGC TGGCGAACGG CGACGAGGTC CAGATCGGCA AGCTCCGGTT GGTGTTCTTG	420
ACCGGACCCA AGCAAGGCGA GGATGACGGG AGTACCGGGG GCCCGTGAGC GCACCCGATA	480
GCCCCGCGCT GGCCGGGATG TCGATCGGGG CGGTCTCTCC ACCTGCTACG ACCGGATTTT	540
CCCTGATGTC CACCATCTCC AAGATTTCGAT TCTTGGGAGG CTTGAGGGTC NGGGTGACCC	600
CCCCGCGGGC CTCATTCTNGG GGTNTCGGCN GGTTCACCC CNTACCNACT GCCNCCCGGN	660
TTGCNAATTC NTTCTTCNCT GCCCNAAAG GGACNNTAN CTTGCCGCTN GAAANGGTNA	720
TCCNGGGCCC NTCCTNGAAN CCCCNTCCCC CT	752

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CATATGCATC ACCATCACCA TCACACTTCT AACCGCCCAG CGCGTCGGGG GCGTCGAGCA	60
CCACGCGACA CCGGGCCCGA TCGATCTGCT AGCTTGAGTC TGGTCAGGCA TCGTCGTCAG	120
CAGCGCGATG CCCTATGTTT GTCGTCGACT CAGATATCGC GGCAATCCAA TCTCCCGCCT	180
GCGGCCGGCG GTGCTGCAAA CTACTCCCGG AGGAATTTTCG ACGTGCGCAT CAAGATCTTC	240
ATGCTGGTCA CGGCTGTCGT TTTGCTCTGT TGTTCGGGTG TGGCCACGGC CGCGCCCAAG	300
ACCTACTGCG AGGAGTTGAA AGGCACCGAT ACCGGCCAGG CGTGCCAGAT TCAAATGTCC	360
GACCCGGCCT ACAACATCAA CATCAGCCTG CCCAGTTACT ACCCCGACCA GAAGTCGCTG	420
GAAAATTACA TCGCCCAGAC GCGCGACAAG TTCCTCAGCG CGGCCACATC GTCCACTCCA	480
CGCGAAGCCC CCTACGAATT GAATATCACC TCGGCCACAT ACCAGTCCGC GATACCGCCG	540
CGTGGTACGC AGGCCGTGGT GCTCAMGGTC TACCACAACG CCGGCGGCAC GCACCCAACG	600
ACCACGTACA AGGCCTTCGA TTGGGACCAG GCCTATCGCA AGCCAATCAC CTATGACACG	660

CTGTGGCAGG CTGACACCGA TCCGCTGCCA GTCGTCTTCC CCATTGTTGC AAGGTGAACT	720
GAGCAACGCA GACCGGGACA ACWGGTATCG ATAGCCGCCN AATGCCGGCT TGGAACCCNG	780
TGAAATTATC ACAACTTCGC AGTCACNAAA NAA	813

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 447 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGTATGAAC ACGGCCGCGT CCGATAACTT CCAGCTGTCC CAGGGTGGGC AGGGATTTCGC	60
CATTCCGATC GGGCAGGCGA TGGCGATCGC GGGCCAGATC CGATCGGGTG GGGGGTCACC	120
CACCGTTTCAT ATCGGGCCTA CCGCCTTCCT CGGCTTGGGT GTTGTCGACA ACAACGGCAA	180
CGGCGCACGA GTCCAACGCG TGGTCGGGAG CGCTCCGGCG GCAAGTCTCG GCATCTCCAC	240
CGGCGACGTG ATCACCGCGG TCGACGGCGC TCCGATCAAC TCGGCCACCG CGATGGCGGA	300
CGCGCTTAAC GGGCATCATC CCGGTGACGT CATCTCGGTG AACTGGCAAA CCAAGTCGGG	360
CGGCACGCGT ACAGGGAACG TGACATTGGC CGAGGGACCC CCGGCCTGAT TTCGTCGYGG	420
ATACCACCCG CCGGCCGGCC AATTGGA	447

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 604 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTCCCACTGC GGTCGCCGAG TATGTCGCCC AGCAAATGTC TGGCAGCCGC CCAACGGAAT	60
CCGGTGATCC GACGTCGCAG GTTGTCGAAC CCGCCGCCGC GGAAGTATCG GTCCATGCCT	120
AGCCCGGCGA CGGCGAGCGC CGGAATGGCG CGAGTGAGGA GGCGGGCAAT TTGGCGGGGC	180
CCGGCGACGG NGAGCGCCGG AATGGCGCGA GTGAGGAGGT GGNCAATCAT GCCCAGNGTG	240
ATCCAATCAA CCTGNATTCG GNCTGNNGGN CCATTTGACA ATCGAGGTAG TGAGCGCAAA	300
TGAATGATGG AAAACGGGNG GNGACGTCCG NTGTTCTGGT GGTGNTAGGT GNCTGNCTGG	360
NGTNGNGGNT ATCAGGATGT TCTTCGNCGA AANCTGATGN CGAGGAACAG GGTGTNCCCG	420
NNANCCNAN GGNGTCCNAN CCCNNNTTC TCGNCGANAT CANANAGNCG NTTGATGNGA	480
NAAAAGGGTG GANCAGNNNN AANTNGNGGN CCNAANAANC NNNANNGNNG NNAGNTNGNT	540

NNNTNTTNNC ANNNNNNTG NNGNNGNNCN NNNCAANCNN NTNNNNGNAA NNGGNTTNTT 600  
NAAT 604

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 633 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTGCANGTCG AACCACCTCA CTAAAGGGAA CAAAAGCTNG AGCTCCACCG CGGTGGCGGC 60  
 CGCTCTAGAA CTAGTGKATM YYYCKGGCTG CAGSAATYCG GYACGAGCAT TAGGACAGTC 120  
 TAACGGTCCT GTTACGGTGA TCGAATGACC GACGACATCC TGCTGATCGA CACCGACGAA 180  
 CGGGTGCGAA CCCTCACCTT CAACCGGCCG CAGTCCCGYA ACGCGCTCTC GGCGGCGCTA 240  
 CGGGATCGGT TTTTCGCGGY GTTGGYCGAC GCCGAGGYCG ACGACGACAT CGACGTCGTC 300  
 ATCCTCACCG GYGCCGATCC GGTGTTCTGC GCCGACTGG ACCTCAAGGT AGCTGGCCGG 360  
 GCAGACCGCG CTGCCGGACA TCTACCGCG GTGGGCGGCC ATGACCAAGC CGGTGATCGG 420  
 CGCGATCAAC GGCGCCGCG TCACCGCGG GCTCGAACTG GCGCTGTACT GCGACATCCT 480  
 GATCGCCTCC GAGCACGCCC GCTTCGNCGA CACCCACGCC CGGGTGGGGC TGCTGCCCCAC 540  
 CTGGGGACTC AGTGTGTGCT TGCCGCAAAA GGTCGGCATC GGNCTGGGCC GGTGGATGAG 600  
 CCTGACCGGC GACTACCTGT CCGTGACCGA CGC 633

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1362 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGACGACGAC GGCGCCGGAG AGCGGGCGCG AACGGCGATC GACGCGGCCC TGGCCAGAGT 60  
 CGGCACCACC CAGGAGGGAG TCGAATCATG AAATTTGTCA ACCATATTGA GCCCGTCGCG 120  
 CCCC GCCGAG CCGGCGGCG GGTGCGCGAG GTCTATGCCG AGGCCCCGCG CGAGTTCGGC 180  
 CGGCTGCCCC AGCCGCTCGC CATGCTGTCC CCGGACGAGG GACTGCTCAC CGCCGGCTGG 240  
 GCGACGTTGC GCGAGACACT GCTGGTGGGC CAGGTGCCGC GTGGCCGCAA GGAAGCCGTC 300  
 GCCGCCGCCG TCGCGGCCAG CCTGCGCTGC CCCTGGTGCG TCGACGACA CACCACCATG 360  
 CTGTACGCGG CAGGCCAAAC CGACACCGCC GCGGCGATCT TGGCCGGCAC AGCACCTGCC 420

GCCGGTGACC	CGAACGCGCC	GTATGTGGCG	TGGGCGGCAG	GAACCGGGAC	ACCGGCGGGA	480
CCGCCGGCAC	CGTTCGGCCC	GGATGTCGCC	GCCGAATACC	TGGGCACCGC	GGTGCAATTC	540
CACTTCATCG	CACGCCTGGT	CCTGGTGCTG	CTGGACGAAA	CCTTCCTGCC	GGGGGGCCCCG	600
CGCGCCCAAC	AGCTCATGCG	CCGCGCCGGT	GGACTGGTGT	TCGCCCCGAA	GGTGCGCGCG	660
GAGCATCGGC	CGGGCCGCTC	CACCCGCCGG	CTCGAGCCGC	GAACGCTGCC	CGACGATCTG	720
GCATGGGCAA	CACCGTCCGA	GCCCATAGCA	ACCGCGTTCG	CCGCGCTCAG	CCACCACCTG	780
GACACCGCGC	CGCACCTGCC	GCCACCGACT	CGTCAGGTGG	TCAGGCGGGT	CGTGGGGTTCG	840
TGGCACGGCG	AGCCAATGCC	GATGAGCAGT	CGCTGGACGA	ACGAGCACAC	CGCCGAGCTG	900
CCCGCCGACC	TGCACGCGCC	CACCCGTCTT	GCCCTGCTGA	CCGGCCTGGC	CCCGCATCAG	960
GTGACCGACG	ACGACGTCGC	CGCGGCCCGA	TCCCTGCTCG	ACACCGATGC	GGCGCTGGTT	1020
GGCGCCCTGG	CCTGGGCCGC	CTTCACCGCC	GCGCGGCGCA	TCGGCACCTG	GATCGGCGCC	1080
GCCGCCGAGG	GCCAGGTGTC	GCGGCAAAAC	CCGACTGGGT	GAGTGTGCGC	GCCCTGTCCG	1140
TAGGGTGTCA	TCGCTGGCCC	GAGGGATCTC	GCGGCGGCGA	ACGGAGGTGG	CGACACAGGT	1200
GGAAGCTGCG	CCCACTGGCT	TGCGCCCCAA	CGCCGTCTGT	GGCGTTCGGT	TGGCCGCACT	1260
GGCCGATCAG	GTCGGCGCCG	GCCCTTGGCC	GAAGGTCCAG	CTCAACGTGC	CGTCACCGAA	1320
GGACCGGACG	GTCACCGGGG	GTCACCCTGC	GCGCCCCAAG	AA		1362

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCGACGACCC	CGATATGCCG	GGCACCCTAG	CGAAAGCCGT	CGCCGACGCA	CTCGGGCGCG	60
GTATCGCTCC	CGTTGAGGAC	ATTCAGGACT	GCGTGGAGGC	CCGGCTGGGG	GAAGCCGGTC	120
TGGATGACGT	GGCCCGTGTT	TACATCATCT	ACCGGCAGCG	GCGCGCCGAG	CTGCGGACGG	180
CTAAGGCCTT	GCTCGGCGTG	CGGGACGAGT	TAAAGCTGAG	CTTGGCGGCC	GTGACGGTAC	240
TGCGCGAGCG	CTATCTGCTG	CACGACGAGC	AGGGCCGGCC	GGCCGAGTCG	ACCGGCGAGC	300
TGATGGACCG	ATCGGCGCGC	TGTGTCGCGG	CGGCCGAGGA	CCAGTATGAG	CCGGGCTCGT	360
CGAGGCGGTG	GGCCGAGCGG	TTCGCCACGC	TATTACGCAA	CCTGGAATTC	CTGCCGAATT	420
CGCCCACGTT	GATGAACTCT	GGCACCAGCC	TGGGACTGCT	CGCCGGCTGT	TTTGTCTGTC	480
CGATTGAGGA	TTCGCTGCAA	TCGATCTTTG	CGACGCTGGG	ACAGGCCGCC	GAGCTGCAGC	540

GGGCTGGAGG	CGGCACCGGA	TATGCGTTCA	GCCACCTGCG	ACCCGCCGGG	GATCGGGTGG	600
CCTCCACGGG	CGGCACGGCC	AGCGGACCGG	TGTCGTTTCT	ACGGCTGTAT	GACAGTGCCG	660
CGGGTGTGGT	CTCCATGGGC	GGTCGCCGGC	GTGGCGCCTG	TATGGCTGTG	CTTGATGTGT	720
CGCACCCGGA	TATCTGTGAT	TTCGTACCG	CCAAGGCCGA	ATCCCCCAGC	GAGCTCCCGC	780
ATTTCAACCT	ATCGGTTGGT	GTGACCGACG	CGTTCCTGCG	GGCCGTCGAA	CGCAACGGCC	840
TACACCGGCT	GGTCAATCCG	CGAACCGGCA	AGATCGTCGC	GCGGATGCCC	GCCGCCGAGC	900
TGTTGACGCG	CATCTGCAAA	GCCGCGCACG	CCGGTGGCGA	TCCCGGGCTG	GTGTTTCTCG	960
ACACGATCAA	TAGGGCAAAC	CCGGTGCCGG	GGAGAGGCCG	CATCGAGGCG	ACCAACCCGT	1020
GCGGGGAGGT	CCCCTGCTG	CCTTACGAGT	CATGTAATCT	CGGCTCGATC	AACCTCGCCC	1080
GGATGCTCGC	CGACGGTCGC	GTCGACTGGG	ACCGGCTCGA	GGAGGTCGCC	GGTGTGGCGG	1140
TGCGGTTTCT	TGATGACGTC	ATCGATGTCA	GCCGCTACCC	CTTCCCCGAA	CTGGGTGAGG	1200
CGGCCCCGCG	CACCCGCAAG	ATCGGGCTGG	GAGTCATGGG	TTTGGCGGAA	CTGCTTGCCG	1260
CACTGGGTAT	TCCGTACGAC	AGTGAAGAAG	CCGTGCGGTT	AGCCACCCGG	CTCATGCGTC	1320
GCATACAGCA	GGCGGCGCAC	ACGGCATCGC	GGAGGCTGGC	CGAAGAGCGG	GGCGCATTC	1380
CGGCGTTTAC	CGATAGCCGG	TTCGCGCGGT	CGGGCCCCGAG	GCGCAACGCA	CAGGTCACCT	1440
CCGTCGCTCC	GACGGGCA					1458

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 862 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACGGTGTAAT	CGTGCTGGAT	CTGGAACCGC	GTGGCCCCGCT	ACCTACCGAG	ATCTACTGGC	60
GGCGCAGGGG	GCTGGCCCTG	GGCATCGCGG	TCGTCGTAGT	CGGGATCGCG	GTGGCCATCG	120
TCATCGCCTT	CGTCGACAGC	AGCGCCGGTG	CCAAACCCGGT	CAGCGCCGAC	AAGCCGGCCT	180
CCGCCCAGAG	CCATCCGGGC	TCGCCGGCAC	CCCAAGCACC	CCAGCCGGCC	GGGCAAACCG	240
AAGGTAACGC	CGCCGCGGCC	CCGCCGCAGG	GCCAAAACCC	CGAGACACCC	ACGCCCACCG	300
CCGCGGTGCA	GCCGCCGCCG	GTGCTCAAGG	AAGGGGACGA	TTGCCCCGAT	TCGACGCTGG	360
CCGTCAAAGG	TTTGACCAAC	GCGCCGCAGT	ACTACGTCGG	CGACCAGCCG	AAGTTCACCA	420
TGGTGGTCAC	CAACATCGGC	CTGGTGTCTT	GTAAACGCGA	CGTTGGGGCC	GCGGTGTTGG	480
CCGCCTACGT	TTACTCGCTG	GACAACAAGC	GGTTGTGGTC	CAACCTGGAC	TGCGCGCCCT	540

CGAATGAGAC GCTGGTCAAG ACGTTTTCCC CCGGTGAGCA GGTAACGACC GCGGTGACCT	600
GGACCGGGAT GGGATCGGCG CCGCGCTGCC CATTGCCGCG GCCGGCGATC GGGCCGGGCA	660
CCTACAATCT CGTGGTACAA CTGGGCAATC TGCCTCGCT GCCGGTCCG TTCATCCTGA	720
ATCAGCCGCC GCCGCCGCC GGGCCGGTAC CCGCTCCGGG TCCAGCGCAG GCGCCTCCGC	780
CGGAGTCTCC CGCGCAAGGC GGATAATTAT TGATCGCTGA TGGTCGATTC CGCCAGCTGT	840
GACAACCCCT CGCCTCGTGC CG	862

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 622 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTGATCAGCA CCGGCAAGGC GTCACATGCC TCCCTGGGTG TGCAGGTGAC CAATGACAAA	60
GACACCCCGG GCGCCAAGAT CGTCGAAGTA GTGGCCGGTG GTGCTGCCGC GAACGCTGGA	120
GTGCCGAAGG GCGTCGTTGT CACCAAGGTC GACGACCGCC CGATCAACAG CGCGGACGCG	180
TTGGTTGCCG CCGTGCGGTC CAAAGCGCCG GGCGCCACGG TGGCGCTAAC CTTTCAGGAT	240
CCCTCGGGCG GTAGCCGCAC AGTGCAAGTC ACCCTCGGCA AGGCGGAGCA GTGATGAAGG	300
TCGCCGCGCA GTGTTCAAAG CTCGGATATA CCGTGGCACC CATGGAACAG CGTGCGGAGT	360
TGGTGGTTGG CCGGGCACTT GTCGTCTGTCG TTGACGATCG CACGGCGCAC GGCGATGAAG	420
ACCACAGCGG GCCGCTTGTC ACCGAGCTGC TCACCGAGGC CGGGTTTGTT GTCGACGGCG	480
TGGTGGCGGT GTCGGCCGAC GAGGTCGAGA TCCGAAATGC GCTGAACACA GCGGTGATCG	540
GCGGGGTGGA CCTGGTGGTG TCGGTCGGCG GGACCGNGT GACGNCTCGC GATGTCACCC	600
CGGAAGCCAC CCGNGACATT CT	622

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1200 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCGCAGCGG TAAGCCTGTT GGCCGCCGGC AACTGGTGT TGACAGCATG CGGCGGTGGC	60
ACCAACAGCT CGTCGTCAGG CGCAGGCGGA ACGTCTGGGT CGGTGCACTG CGGCGGCAAG	120
AAGGAGCTCC ACTCCAGCGG CTCGACCGCA CAAGAAAATG CCATGGAGCA GTTCGTCTAT	180



GCCTACGTGC	GATCGTGCCC	GGGCTACACG	TTGGACTACA	ACGCCAACGG	GTCCGGTGCC	240
GGGGTGACCC	AGTTTCTCAA	CAACGAAACC	GATTTTCGCCG	GCTCGGATGT	CCCGTTGAAT	300
CCGTCGACCG	GTCAACCTGA	CCGGTCGGCG	GAGCGGTGCG	GTTCCCCGGC	ATGGGACCTG	360
CCGACGGTGT	TCGGCCCCGAT	CGCGATCACC	TACAATATCA	AGGGCGTGAG	CACGCTGAAT	420
CTTGACGGAC	CCACTACCGC	CAAGATTTTC	AACGGCACCA	TCACCGTGTG	GAATGATCCA	480
CAGATCCAAG	CCCTCAACTC	CGGCACCGAC	CTGCCGCCAA	CACCGATTAG	CGTTATCTTC	540
CGCAGCGACA	AGTCCGGTAC	GTCCGACAAC	TTCCAGAAAT	ACCTCGACGG	TGTATCCAAC	600
GGGGCGTGGG	GCAAAGGCGC	CAGCGAAACG	TTCAGCGGGG	GCGTCGGCGT	CGGCGCCAGC	660
GGGAACAACG	GAACGTCGGC	CCTACTGCAG	ACGACCGACG	GGTCGATCAC	CTACAACGAG	720
TGGTCGTTTG	CGGTGGGTAA	GCAGTTGAAC	ATGGCCCAGA	TCATCACGTC	GGCGGGTCCG	780
GATCCAGTGG	CGATCACCAC	CGAGTCGGTC	GGTAAGACAA	TCGCCGGGGC	CAAGATCATG	840
GGACAAGGCA	ACGACCTGGT	ATTGGACACG	TCGTCTGTTCT	ACAGACCCAC	CCAGCCTGGC	900
TCTTACCCGA	TCGTGCTGGC	GACCTATGAG	ATCGTCTGCT	CGAAATACCC	GGATGCGACG	960
ACCGGTACTG	CGGTAAGGGC	GTTTATGCAA	GCCGCGATTG	GTCCAGGCCA	AGAAGGCCTG	1020
GACCAATACG	GCTCCATTCC	GTTGCCCAAA	TCGTTCCAAG	CAAAATTGGC	GGCCGCGGTG	1080
AATGCTATTT	CTTGACCTAG	TGAAGGGAAT	TCGACGGTGA	GCGATGCCGT	TCCGCAGGTA	1140
GGGTCGCAAT	TTGGGCCGTA	TCAGCTATTG	CGGCTGCTGG	GCCGAGGCGG	GATGGGCGAG	1200

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCAAGCAGCT	GCAGGTCGTG	CTGTTCGACG	AACTGGGCAT	GCCGAAGACC	AAACGCACCA	60
AGACCGGCTA	CACCACGGAT	GCCGACGCGC	TGCAGTCGTT	GTTGACAAG	ACCGGGCATC	120
CGTTTCTGCA	ACATCTGCTC	GCCCACCGCG	ACGTACCCCG	GCTCAAGGTC	ACCGTCGACG	180
GGTTGCTCCA	AGCGGTGGCC	GCCGACGGCC	GCATCCACAC	CACGTTCAAC	CAGACGATCG	240
CCGCGACCGG	CCGGCTCTCC	TCGACCGAAC	CCAACCTGCA	GAACATCCCG	ATCCGCACCG	300
ACGCGGGCCG	GCGGATCCGG	GACGCGTTTC	TGGTCGGGGA	CGGTTACGCC	GAGTTGATGA	360
CGGCCGACTA	CAGCCAGATC	GAGATGCGGA	TCATGGGGCA	CCTGTCCGGG	GACGAGGGCC	420
TCATCGAGGC	GTTCAACACC	GGGGAGGACC	TGTATTTCGTT	CGTCGCGTCC	CGGGTGTTCG	480

GTGTGCCCCAT	CGACGAGGTC	ACCGGCGAGT	TGCGGCGCCG	GGTCAAGGCG	ATGTCCTACG	540
GGCTGGTTTA	CGGGTTGAGC	GCCTACGGCC	TGTCGCAGCA	GTTGAAAATC	TCCACCGAGG	600
AAGCCAACGA	GCAGATGGAC	GCGTATTTTCG	CCCGATTTCGG	CGGGGTGCGC	GA CTACCTGC	660
GCGCCGTAGT	CGAGCGGGCC	CGCAAGGACG	GCTACACCTC	GACGGTGCTG	GGCCGTGCGC	720
GCTACCTGCC	CGAGCTGGAC	AGCAGCAACC	GTCAAGTGCG	GGAGGCCGCC	GAGCGGGCGG	780
CGCTGAACGC	GCCGATCCAG	GGCAGCGCGG	CCGACATCAT	CAAGGTGGCC	ATGATCCAGG	840
TCGACAAGGC	GCTCAACGAG	GCACAGCTGG	CGTCGCGCAT	GCTGCTGCAG	GTCCACGACG	900
AGCTGCTGTT	CGAAAATCGCC	CCCGGTGAAC	GCGAGCGGGT	CGAGGCCCTG	GTGCGCGACA	960
AGATGGGCGG	CGCTTACCCG	CTCGACGTCC	CGCTGGAGGT	GTCGGTGGGC	TACGGCCGCA	1020
GCTGGGACGC	GGCGGCGCAC	TGAGTGCCGA	GCGTG CATCT	GGGGCGGGAA	TTCGGCGATT	1080
TTTCCGCCCT	GAGTTCACGC	TCGGCGCAAT	CGGGACCGAG	TTTGTCCAGC	GTGTACCCGT	1140
CGAGTAGCCT	CGTCA					1155

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGCGCCGTC	TGGTGTTTGA	ACGGTTTTAC	CGGTCGGCAT	CGGCACGGGC	GTTGCCGGGT	60
TCGGGCCTCG	GGTTGGCGAT	CGTCAAACAG	GTGGTGCTCA	ACCACGGCGG	ATTGCTGCGC	120
ATCGAAGACA	CCGACCCAGG	CGGCCAGCCC	CCTGGAACGT	CGATTTACGT	GCTGCTCCCC	180
GGCCGTCGGA	TGCCGATTCC	GCAGCTTCCC	GGTGCGACGG	CTGGCGCTCG	GAGCACGGAC	240
ATCGAGAACT	CTCGGGGTTC	GGCGAACGTT	ATCTCAGTGG	AATCTCAGTC	CACGCGCGCA	300
ACCTAGTTGT	GCAGTTACTG	TTGAAAGCCA	CACCCATGCC	AGTCCACGCA	TGGCCAAGTT	360
GGCCCGAGTA	GTGGGCCTAG	TACAGGAAGA	GCAACCTAGC	GACATGACGA	ATCACCCACG	420
GTATTGCGCA	CCGCCGCAGC	AGCCGGGAAC	CCCAGGTTAT	GCTCAGGGGC	AGCAGCAAAC	480
GTACAGCCAG	CAGTTCGACT	GGCGTTACCC	ACCGTCCCCG	CCCCCGCAGC	CAACCCAGTA	540
CCGTCAACCC	TACGAGGCGT	TGGGTGGTAC	CCGGCCGGGT	CTGATACCTG	GCGTGATTCC	600
GACCATGACG	CCCCCTCCTG	GGATGGTTTCG	CCAACGCCCT	CGTGCAGGCA	TGTTGGCCAT	660
CGGCGCGGTG	ACGATAGCGG	TGGTGTCCGC	CGGCATCGGC	GGCGCGGCCG	CATCCCTGGT	720
CGGGTTCAAC	CGGGCACCCG	CCGGCCCCAG	CGGCGGCCCA	GTGGCTGCCA	GCGCGGCGCC	780

AAGCATCCCC	GCAGCAAACA	TGCCGCCGGG	GTCTGGTCGAA	CAGGTGGCGG	CCAAGGTGGT	840
GGCCAGTGTC	GTCATGTTGG	AAACCGATCT	GGGCCGCCAG	TCGGAGGAGG	GCTCCGGCAT	900
CATTCTGTCT	GCCGAGGGGC	TGATCTTGAC	CAACAACCAC	GTGATCGCGG	CGGCCGCCAA	960
GCCTCCCCTG	GGCAGTCCGC	CGCCGAAAAC	GACGGTAACC	TTCTCTGACG	GGCGGACCGC	1020
ACCCTTCACG	GTGGTGGGGG	CTGACCCAC	CAGTGATATC	GCCGTCTGTC	GTGTTTCAGG	1080
CGTCTCCGGG	CTCACCCCGA	TCTCCCTGGG	TTCCTCCTCG	GACCTGAGGG	TCGGTCAGCC	1140
GGTGCTGGCG	ATCGGGTCGC	CGCTCGGTTT	GGAGGGCACC	GTGACCACGG	GGATCGTCAG	1200
CGCTCTCAAC	CGTCCAGTGT	CGACGACCGG	CGAGGCCGGC	AACCAGAACA	CCGTGCTGGA	1260
CGCCATTGAG	ACCGACGCCG	CGATCAACCC	CGGTAAGTCC	GGGGGCGCGC	TGGTGAACAT	1320
GAACGCTCAA	CTCGTCGGAG	TCAACTCGGC	CATTGCCACG	CTGGGCGCGG	ACTCAGCCGA	1380
TGCGCAGAGC	GGCTCGATCG	GTCTCGGTTT	TGCGATTCCA	GTGACCAGG	CCAAGCGCAT	1440
CGCCGACGAG	TTGATCAGCA	CCGGCAAGGC	GTCACATGCC	TCCCTGGGTG	TGCAGGTGAC	1500
CAATGACAAA	GACACCCCGG	GCGCCAAGAT	CGTCGAAGTA	GTGGCCGGTG	GTGCTGCCGC	1560
GAACGCTGGA	GTGCCGAAGG	GCGTCGTTGT	CACCAAGGTC	GACGACCGCC	CGATCAACAG	1620
CGCGGACGCG	TTGGTTGCCG	CCGTGCGGTC	CAAAGCGCCG	GGCGCCACGG	TGGCGCTAAC	1680
CTTTCAGGAT	CCCTCGGGCG	GTAGCCGCAC	AGTGCAAGTC	ACCCTCGGCA	AGGCGGAGCA	1740
GTGATGAAGG	TCGCCGCGCA	GTGTTCAAAG	C			1771

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTCCACCGCG	GTGGCGGCCG	CTCTAGAACT	AGTGGATCCC	CCGGGCTGCA	GGAATTCGGC	60
ACGAGGATCC	GACGTCGCAG	GTTGTCGAAC	CCGCCGCCGC	GGAAGTATCG	GTCCATGCCT	120
AGCCCCGGCG	CGGCGAGCGC	CGGAATGGCG	CGAGTGAGGA	GGCGGGCAAT	TTGGCGGGGC	180
CCGGCGACGG	CGAGCGCCGG	AATGGCGCGA	GTGAGGAGGC	GGGCAGTCAT	GCCCAGCGTG	240
ATCCAATCAA	CCTGCATTCG	GCCTGCGGGC	CCATTTGACA	ATCGAGGTAG	TGAGCGCAAA	300
TGAATGATGG	AAAACGGGCG	GTGACGTCCG	CTGTTCTGGT	GGTGCTAGGT	GCCTGCCTGG	360
CGTTGTGGCT	ATCAGGATGT	TCTTCGCCGA	AACCTGATGC	CGAGGAACAG	GGTGTTCGGG	420
TGAGCCCGAC	GGCGTCCGAC	CCGCGCTCC	TCGCCGAGAT	CAGGCAGTCG	CTTGATGCGA	480

CAAAAGGGTT GACCAGCGTG CACGTAGCGG TCCGAACAAC CGGGAAAGTC GACAGCTTGC	540
TGGGTATTAC CAGTGCCGAT GTCGACGTCC GGGCCAATCC GCTCGCGGCA AAGGGCGTAT	600
GCACCTACAA CGACGAGCAG GGTGTCCCGT TTCGGGTACA AGGCGACAAC ATCTCGGTGA	660
AACTGTTTCA CGACTGGAGC AATCTCGGCT CGATTTCTGA ACTGTCAACT TCACGCGTGC	720
TCGATCCTGC CGCTGGGGTG ACGCAGCTGC TGTCCGGTGT CACGAACCTC CAAGCGCAAG	780
GTACCGAAGT GATAGACGGA ATTTGACCA CCAAATCAC CGGGACCATC CCCGCGAGCT	840
CTGTCAAGAT GCTTGATCCT GGCGCCAAGA GTGCAAGGCC GGCGACCGTG TGGATTGCCC	900
AGGACGGCTC GCACCACCTC GTCCGAGCGA GCATCGACCT CGGATCCGGG TCGATTGAGC	960
TCACGCAGTC GAAATGGAAC GAACCCGTCA ACGTCGACTA GGCCGAAGTT GCGTCGACGC	1020
GTTGNTCGAA ACGCCCTTGT GAACGGTGTC AACGGNAC	1058

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAATTTCGGCA CGAGAGGTGA TCGACATCAT CGGGACCAGC CCCACATCCT GGGAACAGGC	60
GGCGGCGGAG GCGGTCCAGC GGGCGCGGGA TAGCGTCGAT GACATCCGCG TCGCTCGGGT	120
CATTGAGCAG GACATGGCCG TGGACAGCGC CGGCAAGATC ACCTACCGCA TCAAGCTCGA	180
AGTGTCTGTT AAGATGAGGC CGGCGCAACC GCGCTAGCAC GGGCCGGCGA GCAAGACGCA	240
AAATCGCACG GTTTGCGGTT GATTCGTGCG ATTTTGTGTC TGCTCGCCGA GGCCTACCAG	300
GCGCGGCCCA GGTCCGCGTG CTGCCGTATC CAGGCGTGCA TCGCGATTCC GGCGGCCACG	360
CCGGAGTTAA TGCTTCGCGT CGACCCGAAC TGGGCGATCC GCCGGNGAGC TGATCGATGA	420
CCGTGGCCAG CCCGTCGATG CCCGAGTTGC CCGAGGAAAC GTGCTGCCAG GCCGGTAGGA	480
AGCGTCCGTA GGCGGCGGTG CTGACCGGCT CTGCCTGCGC CCTCAGTGCG GCCAGCGAGC	540
GG	542

## (2) INFORMATION FOR SEQ ID NO:16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 913 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGGTGCCGCC	CGCGCCTCCG	TTGCCCCCAT	TGCCGCCGTC	GCCGATCAGC	TGCGCATCGC	60
CACCATCACC	GCCTTTGCCG	CCGGCACC GC	CGGTGGCGCC	GGGGCCGCCG	ATGCCACCGC	120
TTGACCCTGG	CCGCCGGCGC	CGCCATTGCC	ATACAGCACC	CCGCCGGGGG	CACCGTTACC	180
GCCGTCGCCA	CCGTCGCCGC	CGCTGCCGTT	TCAGGCCGGG	GAGGCCGAAT	GAACCGCCGC	240
CAAGCCCGCC	GCCGGCACC	TTGCCGCCTT	TTCCGCCCGC	CCCGCCGGCG	CCGCCAATTG	300
CCGAACAGCC	AMGCACCGTT	GCCGCCAGCC	CCGCCGCCGT	TAACGGCGCT	GCCGGGCGCC	360
GCCGCCGGAC	CCGCCATTAC	CGCCGTTCCC	GTTCCGGTGCC	CCGCCGTTAC	CGGCGCCGCC	420
GTTTGCCGCC	AATATTCGGC	GGGCACCGCC	AGACCCGCCG	GGGCCACCAT	TGCCGCCGGG	480
CACCGAAACA	ACAGCCCAAC	GGTGCCGCCG	GCCCCGCCGT	TTGCCGCCAT	CACCGGCCAT	540
TCACCGCCAG	CACCGCCGTT	AATGTTTATG	AACCCGGTAC	CGCCAGCGCG	GCCCCATTG	600
CCGGGCGCCG	GAGNGCGTGC	CCGCCGGCGC	CGCCAACGCC	CAAAAGCCCG	GGGTTGCCAC	660
CGGCCCCGCC	GGACCCACCG	GTCCCGCCGA	TCCCCCGTT	GCCGCCGGTG	CCGCCGCCAT	720
TGGTGCTGCT	GAAGCCGTTA	GCGCCGGTTC	CGCSGGTTCC	GGCGGTGGCG	CCNTGGCCGC	780
CGGCCCCGCC	GTTGCCGTAC	AGCCACCCCC	CGGTGGCGCC	GTTGCCGCCA	TTGCCGCCAT	840
TGCCGCCGTT	GCCGCCATTG	CCGCCGTTCC	CGCCGCCACC	GCCGGNTTGG	CCGCCGGCGC	900
CGCCGGCGGC	CGC					913

## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1872 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GACTACGTTG	GTGTAGAAAA	ATCCTGCCGC	CCGGACCCTT	AAGGCTGGGA	CAATTTCTGA	60
TAGTACCCC	GACACAGGAG	GTTACGGGAT	GAGCAATTCG	CGCCGCCGCT	CACTCAGGTG	120
GTCATGGTTG	CTGAGCGTGC	TGGCTGCCGT	CGGGCTGGGC	CTGGCCACGG	CGCCGGCCCA	180
GGCGGCCCCG	CCGGCCTTGT	CGCAGGACCG	GTTCCGCCGAC	TTCCCCGCGC	TGCCCCCTCGA	240
CCCGTCCGCG	ATGGTCGCCC	AAGTGGCGCC	ACAGGTGGTC	AACATCAACA	CCAAACTGGG	300
CTACAACAAC	GCCGTGGGCG	CCGGGACCGG	CATCGTCATC	GATCCCAACG	GTGTCTGTGCT	360
GACCAACAAC	CACGTGATCG	CGGGCGCCAC	CGACATCAAT	GCGTTCAGCG	TCGGCTCCGG	420
CCAAACCTAC	GGCGTCGATG	TGGTCGGGTA	TGACCGCACC	CAGGATGTCTG	CGGTGCTGCA	480

GCTGCGCGGT	GCCGGTGGCC	TGCCGTCGGC	GGCGATCGGT	GGCGGCGTCG	CGGTTGGTGA	540
GCCCCGTCGTC	GCGATGGGCA	ACAGCGGTGG	GCAGGGCGGA	ACGCCCCGTG	CGGTGCCTGG	600
CAGGGTGGTC	GCGCTCGGCC	AAACCGTGCA	GGCGTCGGAT	TCGCTGACCG	GTGCCGAAGA	660
GACATTGAAC	GGGTTGATCC	AGTTCGATGC	CGCAATCCAG	CCCGGTGATT	CGGGCGGGCC	720
CGTCGTCAAC	GGCCTAGGAC	AGGTGGTCGG	TATGAACACG	GCCGCGTCCG	ATAACTTCCA	780
GCTGTCCCAG	GGTGGGCAGG	GATTCGCCAT	TCCGATCGGG	CAGGCGATGG	CGATCGCGGG	840
CCAAATCCGA	TCGGGTGGGG	GGTCACCCAC	CGTTCATATC	GGGCCTACCG	CCTTCCTCGG	900
CTTGGGTGTT	GTCGACAACA	ACGGCAACGG	CGCACGAGTC	CAACGCGTGG	TCGGAAGCGC	960
TCCGGCGGCA	AGTCTCGGCA	TCTCCACCGG	CGACGTGATC	ACCGCGGTCTG	ACGGCGCTCC	1020
GATCAACTCG	GCCACCGCGA	TGGCGGACGC	GCTTAACGGG	CATCATCCCG	GTGACGTCAT	1080
CTCGGTGAAC	TGGCAAACCA	AGTCGGGCGG	CACGCGTACA	GGGAACGTGA	CATTGGCCGA	1140
GGGACCCCCG	GCCTGATTTG	TCGCGGATAC	CACCCGCCGG	CCGGCCAATT	GGATTGGCGC	1200
CAGCCGTGAT	TGCCGCGTGA	GCCCCCGAGT	TCCGTCTCCC	GTGCGCGTGG	CATTGTGGAA	1260
GCAATGAACG	AGGCAGAACA	CAGCGTTGAG	CACCCTCCCG	TGCAGGGCAG	TTACGTCGAA	1320
GGCGGTGTGG	TCGAGCATCC	GGATGCCAAG	GACTTCGGCA	GCGCCGCCGC	CCTGCCCCGC	1380
GATCCGACCT	GGTTTAAGCA	CGCCGTCTTC	TACGAGGTGC	TGGTCCGGGC	GTTCTTCGAC	1440
GCCAGCGCGG	ACGGTTCGCGN	CGATCTGCGT	GGACTCATCG	ATCGCCTCGA	CTACCTGCAG	1500
TGGCTTGGCA	TCGACTGCAT	CTGTTGCCGC	CGTTCCTACG	ACTCACCGCT	GCGCGACGGC	1560
GGTTACGACA	TTCGCGACTT	CTACAAGGTG	CTGCCCCAAT	TCGGCACCGT	CGACGATTTC	1620
GTCGCCCTGG	TCGACACCGC	TCACCGGCGA	GGTATCCGCA	TCATCACCGA	CCTGGTGATG	1680
AATCACACCT	CGGAGTCGCA	CCCCTGGTTT	CAGGAGTCCC	GCCGCGACCC	AGACGGACCG	1740
TACGGTGACT	ATTACGTGTG	GAGCGACACC	AGCGAGCGCT	ACACCGACGC	CCGGATCATC	1800
TTCGTCGACA	CCGAAGAGTC	GAAGTGGTCA	TTCGATCCTG	TCCGCCGACA	GTTNCTACTG	1860
GCACCGATTC	TT					1872

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTTCGCCGAA	ACCTGATGCC	GAGGAACAGG	GTGTTCCCGT	GAGCCCGACG	GCGTCCGACC	60
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CCGCGCTCCT	CGCCGAGATC	AGGCAGTCGC	TTGATGCGAC	AAAAGGGTTG	ACCAGCGTGC	120
ACGTAGCGGT	CCGAACAACC	GGGAAAGTCG	ACAGCTTGCT	GGGTATTACC	AGTGCCGATG	180
TCGACGTCCG	GGCCAATCCG	CTCGCGGCAA	AGGGCGTATG	CACCTACAAC	GACGAGCAGG	240
GTGTCCCGTT	TCGGGTACAA	GGCGACAACA	TCTCGGTGAA	ACTGTTTCGAC	GACTGGAGCA	300
ATCTCGGCTC	GATTTCTGAA	CTGTCAACTT	CACGCGTGCT	CGATCCTGCC	GCTGGGGTGA	360
CGCAGCTGCT	GTCCGGTGTC	ACGAACCTCC	AAGCGCAAGG	TACCGAAGTG	ATAGACGGAA	420
TTTCGACCAC	CAAAATCACC	GGGACCATCC	CCGCGAGCTC	TGTCAAGATG	CTTGATCCTG	480
GCGCCAAGAG	TGCAAGGCCG	GCGACCGTGT	GGATTGCCCA	GGACGGCTCG	CACCACCTCG	540
TCCGAGCGAG	CATCGACCTC	GGATCCGGGT	CGATTGAGCT	CACGCAGTCG	AAATGGAACG	600
AACCCGTCAA	CGTCGACTAG	GCCGAAGTTG	CGTCGACGCG	TTGCTCGAAA	CGCCCTTGTG	660
AACGGTGTCA	ACGGCACCCG	AAAAGTACC	CCCTGACGGC	ATCTGAAAAT	TGACCCCTTA	720
GACCGGGCGG	TTGGTGGTTA	TTCTTCGGTG	GTTCCGGCTG	GTGGGACGCG	GCCGAGGTG	780
CGGTCTTTGA	GCCGGTAGCT	GTCGCCTTTG	AGGGCGACGA	CTTCAGCATG	GTGGACGAGG	840
CGGTGATCA	TGGCGGCAGC	AACGACGTCG	TCGCCGCCGA	AAACCTCGCC	CCACCGGCCG	900
AAGGCCTTAT	TGGACGTGAC	GATCAAGCTG	GCCCCTCAT	ACCGGGAGGA	CACCAGCTGG	960
AAGAAGAGGT	TGGCGGCCTC	GGGCTCAAAC	GGAATGTAAC	CGACTTCGTC	AACCACCAGG	1020
AGCGGATAGC	GGCCAAACCG	GGTGAGTTG	GCGTAGATGC	GCCCGGCGTG	GTGAGCCTCG	1080
GCGAACCGTG	CTACCCATTC	GGCGGCGGTG	GCGAACAGCA	CCCGATGACC	GGCCTGACAC	1140
GCGCGTATCG	CCAGGCCGAC	CGCAAGATGA	GTCTTCCCGG	TGCCAGGCGG	GGCCCAAAAA	1200
CACGACGTTA	TCGCGGGCGG	TGATGAAATC	CAGGGTGCCC	AGATGTGCGA	TGGTGTGCGG	1260
TTTGAGGCCA	CGAGCATGCT	CAAAGTCGAA	CTCTTCCAAC	GACTTCCGAA	CCGGGAAGCG	1320
GGCGGCGCGG	ATGCGGCCCT	CACCACCATG	GGACTCCCGG	GCTGACACTT	CCCCTGCAG	1380
GCAGGCGGCC	AGGTATTCTT	CGTGGCTCCA	GTTCTCGGCG	CGGGCGCGAT	CGGCCAGCCG	1440
GGACACTGAC	TCACGCAGGG	TGGGAGCTTT	CAATGCTCTT	GT		1482

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAATTCGGCA	CGAGCCGGCG	ATAGCTTCTG	GGCCGCGGCC	GACCAGATGG	CTCGAGGGTT	60
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CGTGCTCGGG	GCCACCGCCG	GGCGCACCAC	CCTGACCGGT	GAGGGCCTGC	AACACGCCGA	120
CGGTCACTCG	TTGCTGCTGG	ACGCCACCAA	CCCGGCGGTG	GTTGCCTACG	ACCCGGCCTT	180
CGCCTACGAA	ATCGGCTACA	TCGNNGAAAG	CGGACTGGCC	AGGATGTGCG	GGGAGAACCC	240
GGAGAACATC	TTCTTCTACA	TCACCGTCTA	CAACGAGCCG	TACGTGCAGC	CGCCGGAGCC	300
GGAGAACTTC	GATCCCGAGG	GCGTGCTGGG	GGGTATCTAC	CGNTATCACG	CGGCCACCGA	360
GCAACGCACC	AACAAGNGC	AGATCCTGGC	CTCCGGGGTA	GCGATGCCCC	CGGCGCTGCG	420
GGCAGCACAG	ATGCTGGCCG	CCGAGTGGGA	TGTCGCCGCC	GACGTGTGGT	CGGTGACCAG	480
TTGGGGCGAG	CTAAACCGCG	ACGGGGTGGT	CATCGAGACC	GAGAAGCTCC	GCCACCCCGA	540
TCGGCCGGCG	GGCGTGCCCT	ACGTGACGAG	AGCGCTGGAG	AATGCTCGGG	GCCCCGGTGAT	600
CGCGGTGTCT	GACTGGATGC	GCGCGGTCCC	CGAGCAGATC	CGACCGTGGG	TGCCGGGCAC	660
ATACCTCACG	TTGGGCACCG	ACGGGTTCGG	TTTTTCCGAC	ACTCGGCCCC	CCGGTCGTCT	720
TTACTTCAAC	ACCGACGCCG	AATCCCAGGT	TGGTCGCGGT	TTTGGGAGGG	GTTGGCCGGG	780
TCGACGGGTG	AATATCGACC	CATTCGGTGC	CGGTCGTGGG	CCGCCCCGCC	AGTTACCCGG	840
ATTTCGACGAA	GGTGGGGGGT	TGCGCCCGAN	TAAGTT			876

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1021 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATCCCCCGG	GCTGCAGGAA	TTCGGCACGA	GAGACAAAAT	TCCACGCGTT	AATGCAGGAA	60
CAGATTCATA	ACGAATTCAC	AGCGGCACAA	CAATATGTCT	CGATCGCGGT	TTATTTTCGAC	120
AGCGAAGACC	TGCCGCAGTT	GGCGAAGCAT	TTTTACAGCC	AAGCGGTCGA	GGAACGAAAC	180
CATGCAATGA	TGCTCGTGCA	ACACCTGCTC	GACCGCGACC	TTCGTGTCGA	AATTCCTGGC	240
GTAGACACGG	TGCGAAACCA	GTTCGACAGA	CCCCGCGAGG	CACTGGCGCT	GGCGCTCGAT	300
CAGGAACGCA	CAGTCACCGA	CCAGGTCGGT	CGGCTGACAG	CGGTGGCCCC	CGACGAGGGC	360
GATTTCTCTG	GCGAGCAGTT	CATGCAGTGG	TTCTTGCAGG	AACAGATCGA	AGAGGTGGCC	420
TTGATGGCAA	CCCTGGTGCG	GGTTGCCGAT	CGGGCCGGGG	CCAACCTGTT	CGAGCTAGAG	480
AACTTCGTCT	CACGTGAAGT	GGATGTGGCG	CCGGCCGCAT	CAGGCGCCCC	GCACGCTGCC	540
GGGGGCCGCC	TCTAGATCCC	TGGGGGGGAT	CAGCGAGTGG	TCCCGTTCGC	CCGCCCGTCT	600
TCCAGCCAGG	CCTTGGTGCG	GCCGGGGTGG	TGAGTACCAA	TCCAGGCCAC	CCCGACCTCC	660



CGGNAAAAGT	CGATGTCCTC	GTACTCATCG	ACGTTCCAGG	AGTACACCGC	CCGGCCCTGA	720
GCTGCCGAGC	GGTCAACGAG	TTGCGGATAT	TCCTTTAACG	CAGGCAGTGA	GGGTCCCACG	780
GCGGTTGGCC	CGACCGCCGT	GGCCGCACTG	CTGGTCAGGT	ATCGGGGGGT	CTTGGCGAGC	840
AACAACGTCG	GCAGGAGGGG	TGGAGCCCGC	CGGATCCGCA	GACCGGGGGG	GCGAAAACGA	900
CATCAACACC	GCACGGGATC	GATCTGCGGA	GGGGGGTGCG	GGAATACCGA	ACCGGTGTAG	960
GAGCGCCAGC	AGTTGTTTTT	CCACCAGCGA	AGCGTTTTTCG	GGTCATCGGN	GGCNNTTAAG	1020
T						1021

## (2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CGTGCCGACG	AACGGAAGAA	CACAACCATG	AAGATGGTGA	AATCGATCGC	CGCAGGTCTG	60
ACCGCCGCGG	CTGCAATCGG	CGCCGCTGCG	GCCGGTGTGA	CTTCGATCAT	GGCTGGCGGN	120
CCGGTCGTAT	ACCAGATGCA	GCCGGTCGTC	TTCGGCGCGC	CACTGCCGTT	GGACCCGGNA	180
TCCGCCCCTG	ANGTCCCGAC	CGCCGCCAG	TGGACCAGNC	TGCTCAACAG	NCTCGNCGAT	240
CCCAACGTGT	CGTTTGNAA	CAAGGGNAGT	CTGGTCGAGG	GNGGNATCGG	NGGNANCGAG	300
GGNGNGNATC	GNCGANCA	A				321

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TCTTATCGGT	TCCGTTGGC	GACGGTTTTT	GGNGCGGGT	GGTTAACCCG	CTCGGCCAGC	60
CGATCGACGG	GCGCGGAGAC	GTCGACTCCG	ATACTCGGCG	CGCGCTGGAG	CTCCAGGCGC	120
CCTCGGTGGT	GNACCGGCAA	GGCGTGAAGG	AGCCGTTGNA	GACCGGGATC	AAGGCGATTG	180
ACGCGATGAC	CCCGATCGGC	CGCGGGCAGC	GCCAGCTGAT	CATCGGGGAC	CGCAAGACCG	240
GCAAAAACCG	CCGTCTGTGT	CGGACACCAT	CCTCAAACCA	GCGGGAAGAA	CTGGGAGTCC	300
GGTGGATCCC	AAGAAGCAGG	TGCGCTTGTTG	TATACGTTGG	CCATCGGGCA	AGAAGGGGAA	360
CTTACCATCG	CCG					373

## (2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 352 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

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GTGACGCCGT GATGGGATTC CTGGGCGGGG CCGGTCCGCT GCGGGTGGTG GATCAGCAAC      60
TGGTTACCCG GGTGCCGCAA GGCTGGTCGT TTGCTCAGGC AGCCGCTGTG CCGGTGGTGT      120
TCTTGACGGC CTGGTACGGG TTGGCCGATT TAGCCGAGAT CAAGGCGGGC GAATCGGTGC      180
TGATCCATGC CCGTACCGGC GGTGTGGGCA TGGCGGCTGT GCAGCTGGCT CGCCAGTGGG      240
GCGTGGAGGT TTTCGTCACC GCCAGCCGTG GNAAGTGGGA CACGCTGCGC GCCATNGNGT      300
TTGACGACGA NCCATATCGG NGATTCCNC ACATNCGAAG TTCCGANGGA GA                352

```

## (2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 726 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```

GAAATCCGCG TTCATTCCGT TCGACCAGCG GCTGGCGATA ATCGACGAAG TGATCAAGCC      60
GCGGTTTCGCG GCGCTCATGG GTCACAGCGA GTAATCAGCA AGTTCTCTGG TATATCGCAC      120
CTAGCGTCCA GTTGCTTGCC AGATCGCTTT CGTACCGTCA TCGCATGTAC CGGTTTCGCGT      180
GCCGCACGCT CATGCTGGCG GCGTGCATCC TGGCCACGGG TGTGGCGGGT CTCGGGGTCG      240
GCGCGCAGTC CGCAGCCCAA ACCGCGCCGG TGCCCGACTA CTACTGGTGC CCGGGGCAGC      300
CTTTCGACCC CGCATGGGGG CCCAACTGGG ATCCCTACAC CTGCCATGAC GACTTCCACC      360
GCGACAGCGA CGGCCCCGAC CACAGCCGCG ACTACCCCGG ACCCATCCTC GAAGGTCCCG      420
TGCTTGACGA TCCCGGTGCT GCGCCGCCGC CCCC GGCTGC CGGTGGCGGC GCATAGCGCT      480
CGTTGACCGG GCCGCATCAG CGAATACGCG TATAAACCCG GCGGTGCCCC CGGCAAGCTA      540
CGACCCCCGG CGGGGCAGAT TTACGCTCCC GTGCCGATGG ATCGCGCCGT CCGATGACAG      600
AAAATAGGCG ACGGTTTTTG CAACCGCTTG GAGGACGCTT GAAGGGAACC TGTCATGAAC      660
GGCGACAGCG CCTCCACCAT CGACATCGAC AAGGTTGTTA CCCGCACACC CGTTCGCCGG      720
ATCGTG                                           726

```

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```

CGCGACGACG ACGAACGTCG GGCCCACCAC CGCCTATGCG TTGATGCAGG CGACCGGGAT      60
GGTCGCCGAC CATATCCAAG CATGCTGGGT GCCCACTGAG CGACCTTTTG ACCAGCCGGG      120
CTGCCCCGATG GCGGCCCGGT GAAGTCATTG CGCCGGGGCT TGTGCACCTG ATGAACCCGA      180
ATAGGGAACA ATAGGGGGGT GATTTGGCAG TTCAATGTCG GGTATGGCTG GAAATCCAAT      240
GGCGGGGCAT GCTCGGCGCC GACCAGGCTC GCGCAGGCGG GCCAGCCCGA ATCTGGAGGG      300
AGCACTCAAT GGCGGCGATG AAGCCCCGGA CCGGCGACGG TCCTTTGGAA GCAACTAAGG      360
AGGGGCGCGG CATTGTGATG CGAGTACCAC TTGAGGGTGG CGGTGCCTG GTCGTCGAGC      420
TGACACCCGA CGAAGCCGCC GCACTGGGTG ACGAACTCAA AGGCGTTACT AGCTAAGACC      480
AGCCCAACGG CGAATGGTCG GCGTTACGCG CACACCTTCC GGTAGATGTC CAGTGTCTGC      540
TCGGCGATGT ATGCCAGGA GAACTCTTGG ATACAGCGCT      580

```

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

AACGGAGGCG CCGGGGGTTT TGGCGGGGCC GGGGCGGTCTG GCGGCAACGG CGGGGCCGGC      60
GGTACCGCCG GGTGTTCGG TGTCGGCGGG GCCGGTGGGG CCGGAGGCAA CGGCATCGCC      120
GGTGTACGG GTACGTCGGC CAGCACACCG GGTGGATCCG      160

```

## (2) INFORMATION FOR SEQ ID NO:27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```

GACACCGATA CGATGGTGAT GTACGCCAAC GTTGTGACA CGCTCGAGGC GTTCACGATC      60
CAGCGCACAC CCGACGGCGT GACCATCGGC GATGCGGCCC CGTTCGCGGA GGCGGCTGCC      120

```

AAGGCGATGG GAATCGACAA GCTGCGGGTA ATTCATACCG GAATGGACCC CGTCGTCGCT	180
GAACGCGAAC AGTGGGACGA CGGCAACAAC ACGTTGGCGT TGGCGCCCGG TGTCGTTGTC	240
GCCTACGAGC GCAACGTACA GACCAACGCC CG	272

## (2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 317 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GCAGCCGGTG GTTCTCGGAC TATCTGCGCA CGGTGACGCA GCGCGACGTG CGCGAGCTGA	60
AGCGGATCGA GCAGACGGAT CGCCTGCCGC GGTTCATGCG CTACCTGGCC GCTATCACCG	120
CGCAGGAGCT GAACGTGGCC GAAGCGGCGC GGGTCATCGG GGTCGACGCG GGGACGATCC	180
GTTCGGATCT GCGTGTTTC GAGACGGTCT ATCTGGTACA TCGCCTGCCC GCCTGGTCGC	240
GGAATCTGAC CGCGAAGATC AAGAAGCGGT CAAAGATCCA CGTCGTCGAC AGTGGCTTCG	300
CGGCCTGGTT GCGCGGG	317

## (2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 182 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GATCGTGGAG CTGTCGATGA ACAGCGTTGC CGGACGCGCG GCGGCCAGCA CGTCGGTGTA	60
GCAGCGCCCG ACCACCTCGC CGGTGGGCAG CATGGTGATG ACCACGTCGG CCTCGGCCAC	120
CGCTTCGGGC GCGCTACGAA ACACGCGAC ACCGTGCGCG GCGGCGCCGG ACGCCGCCGT	180
GG	182

## (2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 308 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GATCGCGAAG TTTGGTGAGC AGGTGGTCGA CGCGAAAGTC TGGGCGCCTG CGAAGCGGGT	60
---	----

CGGCGTTCAC GAGGCGAAGA CACGCCTGTC CGAGCTGCTG CGGCTCGTCT ACGGCGGGCA	120
GAGGTTGAGA TTGCCCGCCG CGGCGAGCCG GTAGCAAAGC TTGTGCCGCT GCATCCTCAT	180
GAGACTCGGC GGTTAGGCAT TGACCATGGC GTGTACCGCG TGCCCGACGA TTTGGACGCT	240
CCGTTGTCAG ACGACGTGCT CGAACGCTTT CACCGGTGAA GCGCTACCTC ATCGACACCC	300
ACGTTTGG	308

## (2) INFORMATION FOR SEQ ID NO:31:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CCGACGACGA GCAACTCACG TGGATGATGG TCGGCAGCGG CATTGAGGAC GGAGAGAATC	60
CGGCCGAAGC TGCCGCGCGG CAAGTGCTCA TAGTGACCGG CCGTAGAGGG CTCCCCCGAT	120
GGCACCGGAC TATTCTGGTG TGCCGCTGGC CGGTAAGAGC GGGTAAAAGA ATGTGAGGGG	180
ACACGATGAG CAATCACACC TACCGAGTGA TCGAGATCGT CGGGACCTCG CCCGACGGCG	240
TCGACGCGGC AATCCAGGGC GGTCTGG	267

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1539 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTCGTGCCGA AAGAATGTGA GGGGACACGA TGAGCAATCA CACCTACCGA GTGATCGAGA	60
TCGTGCGGAC CTCGCCCAGC GGCCTCGACG CGGCAATCCA GGGCGGTCTG GCCCGAGCTG	120
CGCAGACCAT GCGCGCGCTG GACTGGTTCG AAGTACAGTC AATTCGAGGC CACCTGGTCG	180
ACGGAGCGGT CGCGCACTTC CAGGTGACTA TGAAAGTCGG CTTCCGCTGG AGGATTCTTG	240
AACCTTCAAG CGCGGCCGAT AACTGAGGTG CATCATTAAG CGACTTTTCC AGAACATCCT	300
GACGCGCTCG AAACGCGGTT CAGCCGACGG TGGCTCCGCC GAGGCGCTGC CTCCAAAATC	360
CCTGCGACAA TTCGTCGGCG GCGCCTACAA GGAAGTCGGT GCTGAATTCTG TCGGGTATCT	420
GGTCGACCTG TGTGGGCTGC AGCCGGACGA AGCGGTGCTC GACGTCGGCT GCGGCTCGGG	480
GCGGATGGCG TTGCCGCTCA CCGGCTATCT GAACAGCGAG GGACGCTACG CCGGCTTCGA	540
TATCTCGCAG AAAGCCATCG CGTGGTGCCA GGAGCACATC ACCTCGGCGC ACCCCAATT	600

CCAGTTCGAG	GTCTCCGACA	TCTACAAC	TCT	GCTGTACAAC	CCGAAAGGGA	AATACCAGTC	660
ACTAGACTTT	CGCTTTCCAT	ATCCGGATGC	GTC	GTCGTTTCGAT	GTGGTGTTC	TTACCTCGGT	720
GTTACCCAC	ATGTTTCCGC	CGGACGTGGA	GCA	CTACTATCTG	GACGAGATCT	CCCGCGTGCT	780
GAAGCCCGGC	GGACGATGCC	TGTGCACGTA	CTT	CTTCTTGCTC	AATGACGAGT	CGTTAGCCCA	840
CATCGCGGAA	GGAAAGAGTG	CGCACAACTT	CC	CCAGCATGAG	GGACCGGGTT	ATCGGACAAT	900
CCACAAGAAG	CGGCCCCAAG	AAGCAATCGG	CTT	CTTGCCGGAG	ACCTTCGTCA	GGGATGTCTA	960
TGGCAAGTTC	GGCCTCGCCG	TGCACGAACC	ATT	ATTGCACTAC	GGCTCATGGA	GTGGCCGGGA	1020
ACCACGCCCTA	AGCTTCCAGG	ACATCGTCAT	CGC	GACCAAAA	ACCGCGAGCT	AGGTCGGCAT	1080
CCGGGAAGCA	TCGCGACACC	GTGGCGCCGA	GCG	CCGCTGTC	CGGCAGGCCG	ATTAGGCGGG	1140
CAGATTAGCC	CGCCGCGGCT	CCCGGCTCCG	AGT	ACGGCGC	CCCGAATGGC	GTCACCGGCT	1200
GGTAACCACG	CTTGCGCGCC	TGGGCGGCGG	CCT	GCCGGAT	CAGGTGGTAG	ATGCCGACAA	1260
AGCCTGCGTG	ATCGGTCATC	ACCAACGGTG	AC	AGCAGCCG	GTTGTGCACC	AGCGCGAACG	1320
CCACCCCGGT	CTCCGGGTCT	GTCCAGCCGA	TC	GAGCCGCC	CAAGCCCACA	TGACCAAACC	1380
CCGGCATCAC	GTTGCCGATC	GGCATAACGT	GAT	AGCCAAG	ATGAAAATTT	AAGGGCACCA	1440
ATAGATTTTCG	ATCCGGCAGA	ACTTGCCGTC	GGT	TGCGGGT	CAGGCCCCGTG	ACCAGCTCCC	1500
GCGACAAGAA	CCGTATGCCG	TCGATCTCGC	CTC	GTGCCG			1539

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTGCAGGGTG	GCGTGGATGA	GCGTCACCGC	GGGGCAGGCC	GAGCTGACCG	CCGCCCAGGT	60
CCGGGTTGCT	GCGGCGGCCT	ACGAGACGGC	GTATGGGCTG	ACGGTGCCCC	CGCCGGTGAT	120
CGCCGAGAAC	CGTGCTGAAC	TGATGATTCT	GATAGCGACC	AACCTCTTGG	GGCAAAACAC	180
CCCGGCGATC	GCGGTCAACG	AGGCCGAATA	CGGCGAGATG	TGGGCCCAAG	ACGCCGCCGC	240
GATGTTTGGC	TACGCCGCGG	CGACGGCGAC	GGCGACGGCG	ACGTTGCTGC	CGTTCGAGGA	300
GGCGCCGGAG	ATGACCAGCG	CGGGTGGGCT	CCTCGAGCAG	GCCGCCGCGG	TCGAGGAGGC	360
CTCCGACACC	GCCGCGGCGA	ACCAGTTGAT	GAACAATGTG	CCCCAGGCGC	TGAAACAGTT	420
GGCCCAGCCC	ACGCAGGGCA	CCACGCCTTC	TTCCAAGCTG	GGTGGCCTGT	GGAAGACGGT	480
CTCGCCGCAT	CGGTCGCCGA	TCAGCAACAT	GGTGTCGATG	GCCAACAACC	ACATGTTCGAT	540

GACCAACTCG GGTGTGTCGA TGACCAACAC CTTGAGCTCG ATGTTGAAGG GCTTTGCTCC	600
GGCGGCGGCC GCCCAGGCCG TGCAAACCGC GGCGCAAAAC GGGGTCCGGG CGATGAGCTC	660
GCTGGGCAGC TCGCTGGGTT CTTCCGGTCT GGGCGGTGGG GTGGCCGCCA ACTTGGGTCG	720
GGCGGCCTCG GTACGGTATG GTCACCGGGA TGGCGGAAAA TATGCANAGT CTGGTCGGCG	780
GAACGGTGGT CCGGCGTAAG GTTTACCCCC GTTTTCTGGA TCGGTGAAC TTCGTCAACG	840
GAAACAGTTA C	851

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GATCGATCGG GCGGAAATTT GGACCAGATT CGCCTCCGGC GATAACCCAA TCAATCGAAC	60
CTAGATTTAT TCCGTCCAGG GGCCCGAGTA ATGGCTCGCA GGAGAGGAAC CTTACTGCTG	120
CGGGCACCTG TCGTAGGTCC TCGATACGGC GGAAGGCGTC GACATTTTCC ACCGACACCC	180
CCATCCAAAC GTTCGAGGGC CACTCCAGCT TGTGAGCGAG GCGACGCAGT CGCAGGCTGC	240
GCTTGGTCAA GATC	254

## (2) INFORMATION FOR SEQ ID NO:35:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GATCCTGACC GAAGCGGCCG CCGCCAAGGC GAAGTCGCTG TTGGACCAGG AGGGACGGGA	60
CGATCTGGCG CTGCGGATCG CGGTTAGCC GGGGGGGTGC GCTGGATTGC GCTATAACCT	120
TTTCTTCGAC GACCGGACGC TGGATGGTGA CCAAACCGCG GAGTTCGGTG GTGTCAGGTT	180
GATCGTGAC CGGATGAGCG CGCCGTATGT GGAAGGCGCG TCGATCGATT TCGTCGACAC	240
TATTGAGAAG CAAGGTTTAC CATCGACAAT CCCAACGCCA CCGGCTCCTG CGCGTGCGGG	300
GATTCGTTCA ACTGATAAAA CGCTAGTACG ACCCCGCGGT GCGCAACACG TACGAGCACA	360
CCAAGACCTG ACCGCGCTGG AAAAGCAACT GAGCGATGCC TTGCACCTGA CCGCGTGGCG	420
GGCCCGCGG GGCAGGTGTC ACCTGCATGG TGAACAGCAC CTGGGCCTGA TATTGCGACC	480
AGTACACGAT TTTGTCGATC GAGGTCACCT CGACCTGGGA GAACTGCTTG CGGAACGCGT	540

CGCTGCTCAG	CTTGGCCAAG	GCCTGATCGG	AGCGCTTGTC	GCGCACGCCG	TCGTGGATAC	600
CGCACAGCGC	ATTGCGAACG	ATGGTGTCCA	CATCGCGGTT	CTCCAGCGCG	TTGAGGTATC	660
CCTGAATCGC	GGTTTTGGCC	GGTCCCTCCG	AGAATGTGCC	TGCCGTGTTG	GCTCCGTTGG	720
TGCGGACCCC	GATATGATC	GCCGCCGTCA	TAGCCGACAC	CAGCGCGAGG	GCTACCACAA	780
TGCCGATCAG	CAGCCGCTTG	TGCCGTGCT	TCGGGTAGGA	CACCTGCGGC	GGCACGCCGG	840
GATATGCGGC	GGGCGGCAGC	GCCGCGTCGT	CTGCCGGTCC	CGGGGCGAAG	GCCGGTTCGG	900
CGGCGCCGAG	GTCGTGGGGG	TAGTCCAGGG	CTTGGGGTTC	GTGGGATGAG	GGCTCGGGGT	960
ACGGCGCCGG	TCCGTTGGTG	CCGACACCGG	GGTTCGGCGA	GTGGGGACCG	GGCATTGTGG	1020
TTCTCCTAGG	GTGGTGGACG	GGACCAGCTG	CTAGGGCGAC	AACCGCCCGT	CGCGTCAGCC	1080
GGCAGCATCG	GCAATCAGGT	GAGCTCCCTA	GGCAGGCTAG	CGCAACAGCT	GCCGTCAGCT	1140
CTCAACGCGA	CGGGGCGGGC	CGCGGCGCCG	ATAATGTTGA	AAGACTAGGC	AACCTTAGGA	1200
ACGAAGGACG	GAGATTTTGT	GACGATC				1227

## (2) INFORMATION FOR SEQ ID NO:36:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GCGGTGTCGG	CGGATCCGGC	GGGTGGTTGA	ACGGCAACGG	CGGGGCCGGC	GGGGCCGGCG	60
GGACCGGCGC	TAACGGTGGT	GCCGGCGGCA	ACGCCTGGTT	GTTCTGGGGCC	GGCGGGTCCG	120
GCGGNGCCGG	CACCAATGGT	GGNGTCGGCG	GGTCCGGCGG	ATTTGTCTAC	GGCAACGGCG	180
G						181

## (2) INFORMATION FOR SEQ ID NO:37:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCGGTGTCGG	CGGATCCGGC	GGGTGGTTGA	ACGGCAACGG	CGGTGTCGGC	GGCCGGGGCG	60
GCGACGGCGT	CTTTGCCGGT	GCCGGCGGCC	AGGGCGGCCT	CGGTGGGCAG	GGCGGCAATG	120
GCGGCGGCTC	CACCGGCGGC	AACGGCGGTC	TTGGCGGCGC	GGGCGGTGGC	GGAGGCAACG	180
CCCCGGACGG	CGGCTTCGGT	GGCAACGGCG	GTAAGGGTGG	CCAGGGCGGN	ATTGGCGGCG	240



GCACTCAGAG CGCGACCGGC CTCGGNGGTG ACGGCGGTGA CGGCGGTGAC

290

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GATCCAGTGG CATGGNGGGT GTCAGTGGAA GCAT

34

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 155 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GATCGCTGCT CGTCCCCCCC TTGCCGCCGA CGCCACCGGT CCCACCGTTA CCGAACAAGC 60

TGGCGTGGTC GCCAGCACCC CCGGCACCGC CGACGCCGGA GTCGAACAAT GGCACCGTCG 120

TATCCCCACC ATTGCCGCCG GNCCCACCGG CACCG 155

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 53 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ATGGCGTTCA CGGGGCGCCG GGGACCGGGC AGCCCGGNGG GGCCGGGGGG TGG 53

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 132 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GATCCACCGC GGGTGCAGAC GGTGCCCGCG GCGCCACCCC GACCAGCGGC GGCAACGGCG 60

GCACCGGCGG CAACGGCGCG AACGCCACCG TCGTCGGNGG GGCCGGCGGG GCCGGCGGCA 120

AGGGCGGCAA CG 132

## (2) INFORMATION FOR SEQ ID NO:42:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```
GATCGGCGGC CGGNACGGNC GGGGACGGCG GCAAGGGCGG NAACGGGGGC GCCGNAGCCA      60
CCNGCCAAGA ATCCTCCGNG TCCNCCAATG GCGCGAATGG CGGACAGGGC GGCAACGGCG      120
GCANCGGCGG CA                                                              132
```

## (2) INFORMATION FOR SEQ ID NO:43:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```
CGGCACGAGG ATCGGTACCC CGCGGCATCG GCAGCTGCCG ATTCGCCGGG TTTCCCCACC      60
CGAGGAAAGC CGCTACCAGA TGGCGCTGCC GAAGTAGGGC GATCCGTTCG CGATGCCGGC      120
ATGAACGGGC GGCATCAAAT TAGTGCAGGA ACCTTTTCAGT TTAGCGACGA TAATGGCTAT      180
AGCACTAAGG AGGATGATCC GATATGACGC AGTCGCAGAC CGTGACGGTG GATCAGCAAG      240
AGATTTTGAA CAGGGCCAAC GAGGTGGAGG CCCCAGTGGC GGACCCACCG ACTGATGTCC      300
CCATCACACC GTGCGAACTC ACGGNGGNTA AAAACGCCGC CCAACAGNTG GTNTTGTCCG      360
CCGACAACAT GCGGGAATAC CTGGCGGCCG GTGCCAAAGA GCGGCAGCGT CTGGCGACCT      420
CGCTGCGCAA CGCGGCCAAG GNGTATGGCG AGGTTGATGA GGAGGCTGCG ACCGCGCTGG      480
ACAACGACGG CGAAGGAACT GTGCAGGCAG AATCGGCCGG GGCCGTCGGA GGGGACAGTT      540
CGGCCGAACT AACCAGATAC CCGAGGGTGG CCACGGCCGG TGAACCCAAC TTCATGGATC      600
TCAAAGAAGC GGCAAGGAAG CTCGAAACGG GCGACCAAGG CGCATCGCTC GCGCACTGNG      660
GGGATGGGTG GAACACTTNC ACCCTGACGC TGCAAGGCGA CG                                                              702
```

## (2) INFORMATION FOR SEQ ID NO:44:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GAAGCCGCAG	CGCTGTCGGG	CGACGTGGCG	GTCAAAGCGG	CATCGCTCGG	TGGCGGTGGA	60
GGCGGCGGGG	TGCCGTCGGC	GCCGTTGGGA	TCCGCGATCG	GGGCGCCGA	ATCGGTGCGG	120
CCCGCTGGCG	CTGGTGACAT	TGCCGGCTTA	GGCCAGGGAA	GGGCCGGCGG	CGGCGCCGCG	180
CTGGGCGGCG	GTGGCATGGG	AATGCCGATG	GGTGCCGCGC	ATCAGGGACA	AGGGGGCGCC	240
AAGTCCAAGG	GTTCTCAGCA	GGAAGACGAG	GCGCTCTACA	CCGAGGATCC	TCGTGCCG	298

## (2) INFORMATION FOR SEQ ID NO:45:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CGGCACGAGG	ATCGAATCGC	GTCGCCGGGA	GCACAGCGTC	GCACTGCACC	AGTGGAGGAG	60
CCATGACCTA	CTCGCCGGGT	AACCCCGGAT	ACCCGCAAGC	GCAGCCCGCA	GGCTCCTACG	120
GAGGCGTCAC	ACCCTCGTTC	GCCCACGCCG	ATGAGGGTGC	GAGCAAGCTA	CCGATGTACC	180
TGAACATCGC	GGTGGCAGTG	CTCGGTCTGG	CTGCGTACTT	CGCCAGCTTC	GGCCCAATGT	240
TCACCCCTCAG	TACCGAACTC	GGGGGGGGTG	ATGGCGCAGT	GTCCGGTGAC	ACTGGGCTGC	300
CGGTCCGGGT	GGCTCTGCTG	GCTGCGCTGC	TTGCCGGGGT	GGTTCTGGTG	CCTAAGGCCA	360
AGAGCCATGT	GACGGTAGTT	GCGGTGCTCG	GGGTACTCGG	CGTATTTCTG	ATGGTCTCGG	420
CGACGTTTAA	CAAGCCCAGC	GCCTATTCTGA	CCGGTTGGGC	ATTGTGGGTT	GTGTTGGCTT	480
TCATCGTGTT	CCAGGCGGTT	GCGGCAGTCC	TGGCGCTCTT	GGTGGAGACC	GGCGCTATCA	540
CCGCGCCGGC	GCCGCGGCCC	AAGTTCGACC	CGTATGGACA	GTACGGGCGG	TACGGGCAGT	600
ACGGGCAGTA	CGGGGTGCAG	CCGGGTGGGT	ACTACGGTCA	GCAGGGTGCT	CAGCAGGCCG	660
CGGGACTGCA	GTCGCCCCGGC	CCGCAGCAGT	CTCCGCAGCC	TCCCGGATAT	GGGTGCGAGT	720
ACGGCGGCTA	TTCGTCCAGT	CCGAGCCAAT	CGGGCAGTGG	ATACACTGCT	CAGCCCCCGG	780
CCCAGCCGCC	GGCGCAGTCC	GGGTCGCAAC	AATCGCACCA	GGGCCCATCC	ACGCCACCTA	840
CCGGCTTTCC	GAGCTTCAGC	CCACCACCAC	CGGTCACTGC	CGGGACGGGG	TCGCAGGCTG	900
GTTCCGGCTCC	AGTCAACTAT	TCAAACCCCA	GCGGGGGCGA	GCAGTCGTCG	TCCCCCGGGG	960
GGGCGCCGGT	CTAACCAGGC	GTTCCCGCGT	CCGGTCGCGC	GTGTGCGCGA	AGAGTGAACA	1020
GGGTGTCAGC	AAGCGCGGAC	GATCCTCGTG	CCGAATTC			1058

## (2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 327 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```

CGGCACGAGA GACCGATGCC GCTACCCTCG CGCAGGAGGC AGGTAATTTC GAGCGGATCT      60
CCGGCGACCT GAAAACCCAG ATCGACCAGG TGGAGTCGAC GGCAGGTTTC TTGCAGGGCC      120
AGTGGCGCGG CGCGGCGGGG ACGGCCGCCC AGGCCGCGGT GGTGCGCTTC CAAGAAGCAG      180
CCAATAAGCA GAAGCAGGAA CTCGACGAGA TCTCGACGAA TATTCGTCAG GCCGGCGTCC      240
AATACTCGAG GGCCGACGAG GAGCAGCAGC AGGCGCTGTC CTCGCAAATG GGCTTCTGAC      300
CCGCTAATAC GAAAAGAAAC GGAGCAA                                           327

```

## (2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 170 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

```

CGGTCGCGAT GATGGCGTTG TCGAACGTGA CCGATTCTGT ACCGCCGTCG TTGAGATCAA      60
CCAACAACGT GTTGGCGTCG GCAAATGTGC CGNACCCGTG GATCTCGGTG ATCTTGTTCT      120
TCTTCATCAG GAAGTGCACA CCGGCCACCC TGCCCTCGGN TACCTTTCGG                    170

```

## (2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 127 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

```

GATCCGGCGG CACGGGGGGT GCCGGCGGCA GCACCGCTGG CGCTGGCGGC AACGGCGGGG      60
CCGGGGGTGG CGGCGGAACC GGTGGGTTGC TCTTCGGCAA CGGCGGTGCC GGCGGGCACG      120
GGGCCGT                                           127

```

## (2) INFORMATION FOR SEQ ID NO:49:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CGGCGGCAAG GGCGGCACCG CCGGCAACGG GAGCGGCGCG GCCGGCGGCA ACGGCGGCAA 60  
 CGGCGGCTCC GGCCTCAACG G 81

## (2) INFORMATION FOR SEQ ID NO:50:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GATCAGGGCT GGCCGGCTCC GGCCAGAAGG GCGGTAACGG AGGAGCTGCC GGATTGTTTG 60  
 GCAACGGCGG GGCCGGNGGT GCCGGCGCGT CCAACCAAGC CGGTAACGGC GGNGCCGGCG 120  
 GAAACGGTGG TGCCGGTGGG CTGATCTGG 149

## (2) INFORMATION FOR SEQ ID NO:51:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CGGCACGAGA TCACACCTAC CGAGTGATCG AGATCGTCGG GACCTCGCCC GACGGTGTCTG 60  
 ACGCGGNAAT CCAGGGCGGT CTGGCCCGAG CTGCGCAGAC CATGCGCGCG CTGGACTGGT 120  
 TCGAAGTACA GTCAATTCTGA GGCCACCTGG TCGACGGAGC GGTGCGGCAC TTCCAGGTGA 180  
 CTATGAAAGT CGGCTTCCGC CTGGAGGATT CCTGAACCTT CAAGCGCGGC CGATAACTGA 240  
 GGTGCATCAT TAAGCGACTT TTCCAGAACA TCCTGACGCG CTCGAAACGC GGTTCAGCCG 300  
 ACGGTGGCTC CGCCGAGGCG CTGCCTCCAA AATCCCTGCG ACAATTCGTC GGCGG 355

## (2) INFORMATION FOR SEQ ID NO:52:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

```

ATGCATCACC ATCACCATCA CATGCATCAG GTGGACCCCA ACTTGACACG TCGCAAGGGA      60
CGATTGGCGG CACTGGCTAT CGCGGCGATG GCCAGCGCCA GCCTGGTGAC CGTTGCGGTG      120
CCCGCGACCG CCAACGCCGA TCCGGAGCCA GCGCCCCCGG TACCCACAAC GGCCGCCTCG      180
CCGCCGTCGA CCGCTGCAGC GCCACCCGCA CCGGCGACAC CTGTTGCCCC CCCACCACCG      240
GCCGCCGCCA ACACGCCGAA TGCCCAGCCG GGCGATCCCA ACGCAGCACC TCCGCCGGCC      300
GACCCGAACG CACCGCCGCC ACCTGTCATT GCCCCAAACG CACCCCAACC TGTCCGGATC      360
GACAACCCGG TTGGAGGATT CAGCTTCGCG CTGCCTGCTG GCTGGGTGGA GTCTGACGCC      420
GCCCACTTCG ACTACGGTTC AGCACTCCTC AGCAAAACCA CCGGGGACCC GCCATTTCCC      480
GGACAGCCGC CGCCGGTGGC CAATGACACC CGTATCGTGC TCGGCCGGCT AGACCAAAG      540
CTTTACGCCA GCGCCGAAGC CACCGACTCC AAGGCCGCGG CCCGGTTGGG CTCGGACATG      600
GGTGAGTTCT ATATGCCCTA CCCGGGCACC CGGATCAACC AGGAAACCGT CTCGCTCGAC      660
GCCAACGGGG TGTCTGGAAG CGCGTCGTAT TACGAAGTCA AGTTCAGCGA TCCGAGTAAG      720
CCGAACGGCC AGATCTGGAC GGGCGTAATC GGCTCGCCCG CGGCGAACGC ACCGGACGCC      780
GGGCCCCCTC AGCGCTGGTT TGTGGTATGG CTCGGGACCG CCAACAACCC GGTGGACAAG      840
GGCGCGGCCA AGGCGCTGGC CGAATCGATC CGGCCTTTGG TCGCCCCGCC GCCGGCGCCG      900
GCACCGGCTC CTGCAGAGCC CGCTCCGGCG CCGGCGCCGG CCGGGGAAGT CGCTCCTACC      960
CCGACGACAC CGACACCGCA GCGGACCTTA CCGGCCTGA      999

```

## (2) INFORMATION FOR SEQ ID NO:53:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

```

Met His His His His His His Met His Gln Val Asp Pro Asn Leu Thr
1           5           10           15
Arg Arg Lys Gly Arg Leu Ala Ala Leu Ala Ile Ala Ala Met Ala Ser
20           25           30

```

Ala Ser Leu Val Thr Val Ala Val Pro Ala Thr Ala Asn Ala Asp Pro  
 35 40 45  
 Glu Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro Ser Thr  
 50 55 60  
 Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro Val Ala Pro Pro Pro Pro  
 65 70 75 80  
 Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro Gly Asp Pro Asn Ala Ala  
 85 90 95  
 Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro Pro Pro Val Ile Ala Pro  
 100 105 110  
 Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Gly Phe Ser  
 115 120 125  
 Phe Ala Leu Pro Ala Gly Trp Val Glu Ser Asp Ala Ala His Phe Asp  
 130 135 140  
 Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro  
 145 150 155 160  
 Gly Gln Pro Pro Pro Val Ala Asn Asp Thr Arg Ile Val Leu Gly Arg  
 165 170 175  
 Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu Ala Thr Asp Ser Lys Ala  
 180 185 190  
 Ala Ala Arg Leu Gly Ser Asp Met Gly Glu Phe Tyr Met Pro Tyr Pro  
 195 200 205  
 Gly Thr Arg Ile Asn Gln Glu Thr Val Ser Leu Asp Ala Asn Gly Val  
 210 215 220  
 Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys Phe Ser Asp Pro Ser Lys  
 225 230 235 240  
 Pro Asn Gly Gln Ile Trp Thr Gly Val Ile Gly Ser Pro Ala Ala Asn  
 245 250 255  
 Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp Phe Val Val Trp Leu Gly  
 260 265 270  
 Thr Ala Asn Asn Pro Val Asp Lys Gly Ala Ala Lys Ala Leu Ala Glu  
 275 280 285  
 Ser Ile Arg Pro Leu Val Ala Pro Pro Pro Ala Pro Ala Pro Ala Pro  
 290 295 300  
 Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala Gly Glu Val Ala Pro Thr  
 305 310 315 320  
 Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu Pro Ala  
 325 330

## (2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Asp Pro Val Asp Ala Val Ile Asn Thr Thr Xaa Asn Tyr Gly Gln Val  
 1                      5                      10                      15  
 Val Ala Ala Leu  
                     20

## (2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 15 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala Val Glu Ser Gly Met Leu Ala Leu Gly Thr Pro Ala Pro Ser  
 1                      5                      10                      15

## (2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ala Ala Met Lys Pro Arg Thr Gly Asp Gly Pro Leu Glu Ala Ala Lys  
 1                      5                      10                      15  
 Glu Gly Arg

## (2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 15 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Tyr Tyr Trp Cys Pro Gly Gln Pro Phe Asp Pro Ala Trp Gly Pro  
 1                      5                      10                      15



## (2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 14 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Asp Ile Gly Ser Glu Ser Thr Glu Asp Gln Gln Xaa Ala Val  
 1                      5                      10

## (2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 13 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Ala Glu Glu Ser Ile Ser Thr Xaa Glu Xaa Ile Val Pro  
 1                      5                      10

## (2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 17 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Asp Pro Glu Pro Ala Pro Pro Val Pro Thr Ala Ala Ala Ala Pro Pro  
 1                      5                      10                      15  
 Ala

## (2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 15 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Ala Pro Lys Thr Tyr Xaa Glu Glu Leu Lys Gly Thr Asp Thr Gly  
 1                      5                      10                      15

## (2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 30 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

```

Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln Gln Thr Ser
1           5           10           15

Leu Leu Asn Asn Leu Ala Asp Pro Asp Val Ser Phe Ala Asp
          20           25           30

```

## (2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 187 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

```

Thr Gly Ser Leu Asn Gln Thr His Asn Arg Arg Ala Asn Glu Arg Lys
1           5           10           15

Asn Thr Thr Met Lys Met Val Lys Ser Ile Ala Ala Gly Leu Thr Ala
          20           25           30

Ala Ala Ala Ile Gly Ala Ala Ala Ala Gly Val Thr Ser Ile Met Ala
          35           40           45

Gly Gly Pro Val Val Tyr Gln Met Gln Pro Val Val Phe Gly Ala Pro
          50           55           60

Leu Pro Leu Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln
          65           70           75           80

Leu Thr Ser Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala
          85           90           95

Asn Lys Gly Ser Leu Val Glu Gly Gly Ile Gly Gly Thr Glu Ala Arg
          100          105          110

Ile Ala Asp His Lys Leu Lys Lys Ala Ala Glu His Gly Asp Leu Pro
          115          120          125

Leu Ser Phe Ser Val Thr Asn Ile Gln Pro Ala Ala Ala Gly Ser Ala
          130          135          140

Thr Ala Asp Val Ser Val Ser Gly Pro Lys Leu Ser Ser Pro Val Thr
          145          150          155          160

Gln Asn Val Thr Phe Val Asn Gln Gly Gly Trp Met Leu Ser Arg Ala
          165          170          175

```

Ser Ala Met Glu Leu Leu Gln Ala Ala Gly Xaa  
 180 185

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Asp	Glu	Val	Thr	Val	Glu	Thr	Thr	Ser	Val	Phe	Arg	Ala	Asp	Phe	Leu	1	5	10	15
Ser	Glu	Leu	Asp	Ala	Pro	Ala	Gln	Ala	Gly	Thr	Glu	Ser	Ala	Val	Ser	20	25	30	
Gly	Val	Glu	Gly	Leu	Pro	Pro	Gly	Ser	Ala	Leu	Leu	Val	Val	Lys	Arg	35	40	45	
Gly	Pro	Asn	Ala	Gly	Ser	Arg	Phe	Leu	Leu	Asp	Gln	Ala	Ile	Thr	Ser	50	55	60	
Ala	Gly	Arg	His	Pro	Asp	Ser	Asp	Ile	Phe	Leu	Asp	Asp	Val	Thr	Val	65	70	75	80
Ser	Arg	Arg	His	Ala	Glu	Phe	Arg	Leu	Glu	Asn	Asn	Glu	Phe	Asn	Val	85	90	95	
Val	Asp	Val	Gly	Ser	Leu	Asn	Gly	Thr	Tyr	Val	Asn	Arg	Glu	Pro	Val	100	105	110	
Asp	Ser	Ala	Val	Leu	Ala	Asn	Gly	Asp	Glu	Val	Gln	Ile	Gly	Lys	Leu	115	120	125	
Arg	Leu	Val	Phe	Leu	Thr	Gly	Pro	Lys	Gln	Gly	Glu	Asp	Asp	Gly	Ser	130	135	140	
Thr	Gly	Gly	Pro	145															

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Thr	Ser	Asn	Arg	Pro	Ala	Arg	Arg	Gly	Arg	Arg	Ala	Pro	Arg	Asp	Thr	1	5	10	15
Gly	Pro	Asp	Arg	Ser	Ala	Ser	Leu	Ser	Leu	Val	Arg	His	Arg	Arg	Gln	20	25	30	

Gln Arg Asp Ala Leu Cys Leu Ser Ser Thr Gln Ile Ser Arg Gln Ser  
 35 40 45  
 Asn Leu Pro Pro Ala Ala Gly Gly Ala Ala Asn Tyr Ser Arg Arg Asn  
 50 55 60  
 Phe Asp Val Arg Ile Lys Ile Phe Met Leu Val Thr Ala Val Val Leu  
 65 70 75 80  
 Leu Cys Cys Ser Gly Val Ala Thr Ala Ala Pro Lys Thr Tyr Cys Glu  
 85 90 95  
 Glu Leu Lys Gly Thr Asp Thr Gly Gln Ala Cys Gln Ile Gln Met Ser  
 100 105 110  
 Asp Pro Ala Tyr Asn Ile Asn Ile Ser Leu Pro Ser Tyr Tyr Pro Asp  
 115 120 125  
 Gln Lys Ser Leu Glu Asn Tyr Ile Ala Gln Thr Arg Asp Lys Phe Leu  
 130 135 140  
 Ser Ala Ala Thr Ser Ser Thr Pro Arg Glu Ala Pro Tyr Glu Leu Asn  
 145 150 155 160  
 Ile Thr Ser Ala Thr Tyr Gln Ser Ala Ile Pro Pro Arg Gly Thr Gln  
 165 170 175  
 Ala Val Val Leu Xaa Val Tyr His Asn Ala Gly Gly Thr His Pro Thr  
 180 185 190  
 Thr Thr Tyr Lys Ala Phe Asp Trp Asp Gln Ala Tyr Arg Lys Pro Ile  
 195 200 205  
 Thr Tyr Asp Thr Leu Trp Gln Ala Asp Thr Asp Pro Leu Pro Val Val  
 210 215 220  
 Phe Pro Ile Val Ala Arg  
 225 230

## (2) INFORMATION FOR SEQ ID NO:66:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe  
 1 5 10 15  
 Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser  
 20 25 30  
 Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly  
 35 40 45  
 Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val  
 50 55 60

Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val  
65 70 75 80

Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala  
85 90 95

Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp  
100 105 110

Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu  
115 120 125

Gly Pro Pro Ala  
130

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 100 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Val Pro Leu Arg Ser Pro Ser Met Ser Pro Ser Lys Cys Leu Ala Ala  
1 5 10 15

Ala Gln Arg Asn Pro Val Ile Arg Arg Arg Arg Leu Ser Asn Pro Pro  
20 25 30

Pro Arg Lys Tyr Arg Ser Met Pro Ser Pro Ala Thr Ala Ser Ala Gly  
35 40 45

Met Ala Arg Val Arg Arg Arg Ala Ile Trp Arg Gly Pro Ala Thr Xaa  
50 55 60

Ser Ala Gly Met Ala Arg Val Arg Arg Trp Xaa Val Met Pro Xaa Val  
65 70 75 80

Ile Gln Ser Thr Xaa Ile Arg Xaa Xaa Gly Pro Phe Asp Asn Arg Gly  
85 90 95

Ser Glu Arg Lys  
100

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 163 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Met Thr Asp Asp Ile Leu Leu Ile Asp Thr Asp Glu Arg Val Arg Thr  
1 5 10 15

Leu Thr Leu Asn Arg Pro Gln Ser Arg Asn Ala Leu Ser Ala Ala Leu  
 20 25 30  
 Arg Asp Arg Phe Phe Ala Xaa Leu Xaa Asp Ala Glu Xaa Asp Asp Asp  
 35 40 45  
 Ile Asp Val Val Ile Leu Thr Gly Ala Asp Pro Val Phe Cys Ala Gly  
 50 55 60  
 Leu Asp Leu Lys Val Ala Gly Arg Ala Asp Arg Ala Ala Gly His Leu  
 65 70 75 80  
 Thr Ala Val Gly Gly His Asp Gln Ala Gly Asp Arg Arg Asp Gln Arg  
 85 90 95  
 Arg Arg Gly His Arg Arg Ala Arg Thr Gly Ala Val Leu Arg His Pro  
 100 105 110  
 Asp Arg Leu Arg Ala Arg Pro Leu Arg Arg His Pro Arg Pro Gly Gly  
 115 120 125  
 Ala Ala Ala His Leu Gly Thr Gln Cys Val Leu Ala Ala Lys Gly Arg  
 130 135 140  
 His Arg Xaa Gly Pro Val Asp Glu Pro Asp Arg Arg Leu Pro Val Arg  
 145 150 155 160  
 Asp Arg Arg

## (2) INFORMATION FOR SEQ ID NO:69:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met Lys Phe Val Asn His Ile Glu Pro Val Ala Pro Arg Arg Ala Gly  
 1 5 10 15  
 Gly Ala Val Ala Glu Val Tyr Ala Glu Ala Arg Arg Glu Phe Gly Arg  
 20 25 30  
 Leu Pro Glu Pro Leu Ala Met Leu Ser Pro Asp Glu Gly Leu Leu Thr  
 35 40 45  
 Ala Gly Trp Ala Thr Leu Arg Glu Thr Leu Leu Val Gly Gln Val Pro  
 50 55 60  
 Arg Gly Arg Lys Glu Ala Val Ala Ala Ala Val Ala Ala Ser Leu Arg  
 65 70 75 80  
 Cys Pro Trp Cys Val Asp Ala His Thr Thr Met Leu Tyr Ala Ala Gly  
 85 90 95  
 Gln Thr Asp Thr Ala Ala Ala Ile Leu Ala Gly Thr Ala Pro Ala Ala  
 100 105 110

Gly Asp Pro Asn Ala Pro Tyr Val Ala Trp Ala Ala Gly Thr Gly Thr  
 115 120 125  
 Pro Ala Gly Pro Pro Ala Pro Phe Gly Pro Asp Val Ala Ala Glu Tyr  
 130 135 140  
 Leu Gly Thr Ala Val Gln Phe His Phe Ile Ala Arg Leu Val Leu Val  
 145 150 155 160  
 Leu Leu Asp Glu Thr Phe Leu Pro Gly Gly Pro Arg Ala Gln Gln Leu  
 165 170 175  
 Met Arg Arg Ala Gly Gly Leu Val Phe Ala Arg Lys Val Arg Ala Glu  
 180 185 190  
 His Arg Pro Gly Arg Ser Thr Arg Arg Leu Glu Pro Arg Thr Leu Pro  
 195 200 205  
 Asp Asp Leu Ala Trp Ala Thr Pro Ser Glu Pro Ile Ala Thr Ala Phe  
 210 215 220  
 Ala Ala Leu Ser His His Leu Asp Thr Ala Pro His Leu Pro Pro Pro  
 225 230 235 240  
 Thr Arg Gln Val Val Arg Arg Val Val Gly Ser Trp His Gly Glu Pro  
 245 250 255  
 Met Pro Met Ser Ser Arg Trp Thr Asn Glu His Thr Ala Glu Leu Pro  
 260 265 270  
 Ala Asp Leu His Ala Pro Thr Arg Leu Ala Leu Leu Thr Gly Leu Ala  
 275 280 285  
 Pro His Gln Val Thr Asp Asp Asp Val Ala Ala Ala Arg Ser Leu Leu  
 290 295 300  
 Asp Thr Asp Ala Ala Leu Val Gly Ala Leu Ala Trp Ala Ala Phe Thr  
 305 310 315 320  
 Ala Ala Arg Arg Ile Gly Thr Trp Ile Gly Ala Ala Ala Glu Gly Gln  
 325 330 335  
 Val Ser Arg Gln Asn Pro Thr Gly  
 340

## (2) INFORMATION FOR SEQ ID NO:70:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Asp Asp Pro Asp Met Pro Gly Thr Val Ala Lys Ala Val Ala Asp Ala  
 1 5 10 15  
 Leu Gly Arg Gly Ile Ala Pro Val Glu Asp Ile Gln Asp Cys Val Glu  
 20 25 30

Ala Arg Leu Gly Glu Ala Gly Leu Asp Asp Val Ala Arg Val Tyr Ile  
 35 40 45  
 Ile Tyr Arg Gln Arg Arg Ala Glu Leu Arg Thr Ala Lys Ala Leu Leu  
 50 55 60  
 Gly Val Arg Asp Glu Leu Lys Leu Ser Leu Ala Ala Val Thr Val Leu  
 65 70 75 80  
 Arg Glu Arg Tyr Leu Leu His Asp Glu Gln Gly Arg Pro Ala Glu Ser  
 85 90 95  
 Thr Gly Glu Leu Met Asp Arg Ser Ala Arg Cys Val Ala Ala Ala Glu  
 100 105 110  
 Asp Gln Tyr Glu Pro Gly Ser Ser Arg Arg Trp Ala Glu Arg Phe Ala  
 115 120 125  
 Thr Leu Leu Arg Asn Leu Glu Phe Leu Pro Asn Ser Pro Thr Leu Met  
 130 135 140  
 Asn Ser Gly Thr Asp Leu Gly Leu Leu Ala Gly Cys Phe Val Leu Pro  
 145 150 155 160  
 Ile Glu Asp Ser Leu Gln Ser Ile Phe Ala Thr Leu Gly Gln Ala Ala  
 165 170 175  
 Glu Leu Gln Arg Ala Gly Gly Gly Thr Gly Tyr Ala Phe Ser His Leu  
 180 185 190  
 Arg Pro Ala Gly Asp Arg Val Ala Ser Thr Gly Gly Thr Ala Ser Gly  
 195 200 205  
 Pro Val Ser Phe Leu Arg Leu Tyr Asp Ser Ala Ala Gly Val Val Ser  
 210 215 220  
 Met Gly Gly Arg Arg Arg Gly Ala Cys Met Ala Val Leu Asp Val Ser  
 225 230 235 240  
 His Pro Asp Ile Cys Asp Phe Val Thr Ala Lys Ala Glu Ser Pro Ser  
 245 250 255  
 Glu Leu Pro His Phe Asn Leu Ser Val Gly Val Thr Asp Ala Phe Leu  
 260 265 270  
 Arg Ala Val Glu Arg Asn Gly Leu His Arg Leu Val Asn Pro Arg Thr  
 275 280 285  
 Gly Lys Ile Val Ala Arg Met Pro Ala Ala Glu Leu Phe Asp Ala Ile  
 290 295 300  
 Cys Lys Ala Ala His Ala Gly Gly Asp Pro Gly Leu Val Phe Leu Asp  
 305 310 315 320  
 Thr Ile Asn Arg Ala Asn Pro Val Pro Gly Arg Gly Arg Ile Glu Ala  
 325 330 335  
 Thr Asn Pro Cys Gly Glu Val Pro Leu Leu Pro Tyr Glu Ser Cys Asn  
 340 345 350



Leu Gly Ser Ile Asn Leu Ala Arg Met Leu Ala Asp Gly Arg Val Asp  
 355 360 365  
 Trp Asp Arg Leu Glu Glu Val Ala Gly Val Ala Val Arg Phe Leu Asp  
 370 375 380  
 Asp Val Ile Asp Val Ser Arg Tyr Pro Phe Pro Glu Leu Gly Glu Ala  
 385 390 395 400  
 Ala Arg Ala Thr Arg Lys Ile Gly Leu Gly Val Met Gly Leu Ala Glu  
 405 410 415  
 Leu Leu Ala Ala Leu Gly Ile Pro Tyr Asp Ser Glu Glu Ala Val Arg  
 420 425 430  
 Leu Ala Thr Arg Leu Met Arg Arg Ile Gln Gln Ala Ala His Thr Ala  
 435 440 445  
 Ser Arg Arg Leu Ala Glu Glu Arg Gly Ala Phe Pro Ala Phe Thr Asp  
 450 455 460  
 Ser Arg Phe Ala Arg Ser Gly Pro Arg Arg Asn Ala Gln Val Thr Ser  
 465 470 475 480  
 Val Ala Pro Thr Gly  
 485

## (2) INFORMATION FOR SEQ ID NO:71:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Gly Val Ile Val Leu Asp Leu Glu Pro Arg Gly Pro Leu Pro Thr Glu  
 1 5 10 15  
 Ile Tyr Trp Arg Arg Arg Gly Leu Ala Leu Gly Ile Ala Val Val Val  
 20 25 30  
 Val Gly Ile Ala Val Ala Ile Val Ile Ala Phe Val Asp Ser Ser Ala  
 35 40 45  
 Gly Ala Lys Pro Val Ser Ala Asp Lys Pro Ala Ser Ala Gln Ser His  
 50 55 60  
 Pro Gly Ser Pro Ala Pro Gln Ala Pro Gln Pro Ala Gly Gln Thr Glu  
 65 70 75 80  
 Gly Asn Ala Ala Ala Pro Pro Gln Gly Gln Asn Pro Glu Thr Pro  
 85 90 95  
 Thr Pro Thr Ala Ala Val Gln Pro Pro Pro Val Leu Lys Glu Gly Asp  
 100 105 110  
 Asp Cys Pro Asp Ser Thr Leu Ala Val Lys Gly Leu Thr Asn Ala Pro  
 115 120 125

Gln Tyr Tyr Val Gly Asp Gln Pro Lys Phe Thr Met Val Val Thr Asn  
 130 135 140  
 Ile Gly Leu Val Ser Cys Lys Arg Asp Val Gly Ala Ala Val Leu Ala  
 145 150 155 160  
 Ala Tyr Val Tyr Ser Leu Asp Asn Lys Arg Leu Trp Ser Asn Leu Asp  
 165 170 175  
 Cys Ala Pro Ser Asn Glu Thr Leu Val Lys Thr Phe Ser Pro Gly Glu  
 180 185 190  
 Gln Val Thr Thr Ala Val Thr Trp Thr Gly Met Gly Ser Ala Pro Arg  
 195 200 205  
 Cys Pro Leu Pro Arg Pro Ala Ile Gly Pro Gly Thr Tyr Asn Leu Val  
 210 215 220  
 Val Gln Leu Gly Asn Leu Arg Ser Leu Pro Val Pro Phe Ile Leu Asn  
 225 230 235 240  
 Gln Pro Pro Pro Pro Pro Gly Pro Val Pro Ala Pro Gly Pro Ala Gln  
 245 250 255  
 Ala Pro Pro Pro Glu Ser Pro Ala Gln Gly Gly  
 260 265

## (2) INFORMATION FOR SEQ ID NO:72:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Leu Ile Ser Thr Gly Lys Ala Ser His Ala Ser Leu Gly Val Gln Val  
 1 5 10 15  
 Thr Asn Asp Lys Asp Thr Pro Gly Ala Lys Ile Val Glu Val Val Ala  
 20 25 30  
 Gly Gly Ala Ala Ala Asn Ala Gly Val Pro Lys Gly Val Val Val Thr  
 35 40 45  
 Lys Val Asp Asp Arg Pro Ile Asn Ser Ala Asp Ala Leu Val Ala Ala  
 50 55 60  
 Val Arg Ser Lys Ala Pro Gly Ala Thr Val Ala Leu Thr Phe Gln Asp  
 65 70 75 80  
 Pro Ser Gly Gly Ser Arg Thr Val Gln Val Thr Leu Gly Lys Ala Glu  
 85 90 95  
 Gln

## (2) INFORMATION FOR SEQ ID NO:73:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

```

Gly Ala Ala Val Ser Leu Leu Ala Ala Gly Thr Leu Val Leu Thr Ala
1           5           10           15
Cys Gly Gly Gly Thr Asn Ser Ser Ser Ser Gly Ala Gly Gly Thr Ser
          20           25           30
Gly Ser Val His Cys Gly Gly Lys Lys Glu Leu His Ser Ser Gly Ser
          35           40           45
Thr Ala Gln Glu Asn Ala Met Glu Gln Phe Val Tyr Ala Tyr Val Arg
          50           55           60
Ser Cys Pro Gly Tyr Thr Leu Asp Tyr Asn Ala Asn Gly Ser Gly Ala
65           70           75           80
Gly Val Thr Gln Phe Leu Asn Asn Glu Thr Asp Phe Ala Gly Ser Asp
          85           90           95
Val Pro Leu Asn Pro Ser Thr Gly Gln Pro Asp Arg Ser Ala Glu Arg
          100          105          110
Cys Gly Ser Pro Ala Trp Asp Leu Pro Thr Val Phe Gly Pro Ile Ala
          115          120          125
Ile Thr Tyr Asn Ile Lys Gly Val Ser Thr Leu Asn Leu Asp Gly Pro
          130          135          140
Thr Thr Ala Lys Ile Phe Asn Gly Thr Ile Thr Val Trp Asn Asp Pro
          145          150          155          160
Gln Ile Gln Ala Leu Asn Ser Gly Thr Asp Leu Pro Pro Thr Pro Ile
          165          170          175
Ser Val Ile Phe Arg Ser Asp Lys Ser Gly Thr Ser Asp Asn Phe Gln
          180          185          190
Lys Tyr Leu Asp Gly Val Ser Asn Gly Ala Trp Gly Lys Gly Ala Ser
          195          200          205
Glu Thr Phe Ser Gly Gly Val Gly Val Gly Ala Ser Gly Asn Asn Gly
          210          215          220
Thr Ser Ala Leu Leu Gln Thr Thr Asp Gly Ser Ile Thr Tyr Asn Glu
          225          230          235          240
Trp Ser Phe Ala Val Gly Lys Gln Leu Asn Met Ala Gln Ile Ile Thr
          245          250          255
Ser Ala Gly Pro Asp Pro Val Ala Ile Thr Thr Glu Ser Val Gly Lys
          260          265          270

```

```

Thr Ile Ala Gly Ala Lys Ile Met Gly Gln Gly Asn Asp Leu Val Leu
    275                      280                      285

Asp Thr Ser Ser Phe Tyr Arg Pro Thr Gln Pro Gly Ser Tyr Pro Ile
    290                      295                      300

Val Leu Ala Thr Tyr Glu Ile Val Cys Ser Lys Tyr Pro Asp Ala Thr
    305                      310                      315                      320

Thr Gly Thr Ala Val Arg Ala Phe Met Gln Ala Ala Ile Gly Pro Gly
                      325                      330                      335

Gln Glu Gly Leu Asp Gln Tyr Gly Ser Ile Pro Leu Pro Lys Ser Phe
    340                      345                      350

Gln Ala Lys Leu Ala Ala Ala Val Asn Ala Ile Ser
    355                      360

```

## (2) INFORMATION FOR SEQ ID NO:74:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```

Gln Ala Ala Ala Gly Arg Ala Val Arg Arg Thr Gly His Ala Glu Asp
1          5          10          15

Gln Thr His Gln Asp Arg Leu His His Gly Cys Arg Arg Ala Ala Val
    20          25          30

Val Val Arg Gln Asp Arg Ala Ser Val Ser Ala Thr Ser Ala Arg Pro
    35          40          45

Pro Arg Arg His Pro Ala Gln Gly His Arg Arg Arg Val Ala Pro Ser
    50          55          60

Gly Gly Arg Arg Arg Pro His Pro His His Val Gln Pro Asp Asp Arg
    65          70          75          80

Arg Asp Arg Pro Ala Leu Leu Asp Arg Thr Gln Pro Ala Glu His Pro
    85          90          95

Asp Pro His Arg Arg Gly Pro Ala Asp Pro Gly Arg Val Arg Gly Arg
    100         105         110

Gly Arg Leu Arg Arg Val Asp Asp Gly Arg Leu Gln Pro Asp Arg Asp
    115         120         125

Ala Asp His Gly Ala Pro Val Arg Gly Arg Gly Pro His Arg Gly Val
    130         135         140

Gln His Arg Gly Gly Pro Val Phe Val Arg Arg Val Pro Gly Val Arg
    145         150         155         160

Cys Ala His Arg Arg Gly His Arg Arg Val Ala Ala Pro Gly Gln Gly
    165         170         175

```

Asp Val Leu Arg Ala Gly Leu Arg Val Glu Arg Leu Arg Pro Val Ala  
 180 185 190  
 Ala Val Glu Asn Leu His Arg Gly Ser Gln Arg Ala Asp Gly Arg Val  
 195 200 205  
 Phe Arg Pro Ile Arg Arg Gly Ala Arg Leu Pro Ala Arg Arg Ser Arg  
 210 215 220  
 Ala Gly Pro Gln Gly Arg Leu His Leu Asp Gly Ala Gly Pro Ser Pro  
 225 230 235 240  
 Leu Pro Ala Arg Ala Gly Gln Gln Gln Pro Ser Ser Ala Gly Gly Arg  
 245 250 255  
 Arg Ala Gly Gly Ala Glu Arg Ala Asp Pro Gly Gln Arg Gly Arg His  
 260 265 270  
 His Gln Gly Gly His Asp Pro Gly Arg Gln Gly Ala Gln Arg Gly Thr  
 275 280 285  
 Ala Gly Val Ala His Ala Ala Ala Gly Pro Arg Arg Ala Ala Val Arg  
 290 295 300  
 Asn Arg Pro Arg Arg  
 305

## (2) INFORMATION FOR SEQ ID NO:75:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Ser Ala Val Trp Cys Leu Asn Gly Phe Thr Gly Arg His Arg His Gly  
 1 5 10 15  
 Arg Cys Arg Val Arg Ala Ser Gly Trp Arg Ser Ser Asn Arg Trp Cys  
 20 25 30  
 Ser Thr Thr Ala Asp Cys Cys Ala Ser Lys Thr Pro Thr Gln Ala Ala  
 35 40 45  
 Ser Pro Leu Glu Arg Arg Phe Thr Cys Cys Ser Pro Ala Val Gly Cys  
 50 55 60  
 Arg Phe Arg Ser Phe Pro Val Arg Arg Leu Ala Leu Gly Ala Arg Thr  
 65 70 75 80  
 Ser Arg Thr Leu Gly Val Arg Arg Thr Leu Ser Gln Trp Asn Leu Ser  
 85 90 95  
 Pro Arg Ala Gln Pro Ser Cys Ala Val Thr Val Glu Ser His Thr His  
 100 105 110  
 Ala Ser Pro Arg Met Ala Lys Leu Ala Arg Val Val Gly Leu Val Gln  
 115 120 125

Glu	Glu	Gln	Pro	Ser	Asp	Met	Thr	Asn	His	Pro	Arg	Tyr	Ser	Pro	Pro	130	135	140
Pro	Gln	Gln	Pro	Gly	Thr	Pro	Gly	Tyr	Ala	Gln	Gly	Gln	Gln	Gln	Thr	145	150	155
Tyr	Ser	Gln	Gln	Phe	Asp	Trp	Arg	Tyr	Pro	Pro	Ser	Pro	Pro	Pro	Gln	165	170	175
Pro	Thr	Gln	Tyr	Arg	Gln	Pro	Tyr	Glu	Ala	Leu	Gly	Gly	Thr	Arg	Pro	180	185	190
Gly	Leu	Ile	Pro	Gly	Val	Ile	Pro	Thr	Met	Thr	Pro	Pro	Pro	Gly	Met	195	200	205
Val	Arg	Gln	Arg	Pro	Arg	Ala	Gly	Met	Leu	Ala	Ile	Gly	Ala	Val	Thr	210	215	220
Ile	Ala	Val	Val	Ser	Ala	Gly	Ile	Gly	Gly	Ala	Ala	Ala	Ser	Leu	Val	225	230	235
Gly	Phe	Asn	Arg	Ala	Pro	Ala	Gly	Pro	Ser	Gly	Gly	Pro	Val	Ala	Ala	245	250	255
Ser	Ala	Ala	Pro	Ser	Ile	Pro	Ala	Ala	Asn	Met	Pro	Pro	Gly	Ser	Val	260	265	270
Glu	Gln	Val	Ala	Ala	Lys	Val	Val	Pro	Ser	Val	Val	Met	Leu	Glu	Thr	275	280	285
Asp	Leu	Gly	Arg	Gln	Ser	Glu	Glu	Gly	Ser	Gly	Ile	Ile	Leu	Ser	Ala	290	295	300
Glu	Gly	Leu	Ile	Leu	Thr	Asn	Asn	His	Val	Ile	Ala	Ala	Ala	Ala	Lys	305	310	315
Pro	Pro	Leu	Gly	Ser	Pro	Pro	Pro	Lys	Thr	Thr	Val	Thr	Phe	Ser	Asp	325	330	335
Gly	Arg	Thr	Ala	Pro	Phe	Thr	Val	Val	Gly	Ala	Asp	Pro	Thr	Ser	Asp	340	345	350
Ile	Ala	Val	Val	Arg	Val	Gln	Gly	Val	Ser	Gly	Leu	Thr	Pro	Ile	Ser	355	360	365
Leu	Gly	Ser	Ser	Ser	Asp	Leu	Arg	Val	Gly	Gln	Pro	Val	Leu	Ala	Ile	370	375	380
Gly	Ser	Pro	Leu	Gly	Leu	Glu	Gly	Thr	Val	Thr	Thr	Gly	Ile	Val	Ser	385	390	395
Ala	Leu	Asn	Arg	Pro	Val	Ser	Thr	Thr	Gly	Glu	Ala	Gly	Asn	Gln	Asn	405	410	415
Thr	Val	Leu	Asp	Ala	Ile	Gln	Thr	Asp	Ala	Ala	Ile	Asn	Pro	Gly	Asn	420	425	430
Ser	Gly	Gly	Ala	Leu	Val	Asn	Met	Asn	Ala	Gln	Leu	Val	Gly	Val	Asn	435	440	445

Ser Ala Ile Ala Thr Leu Gly Ala Asp Ser Ala Asp Ala Gln Ser Gly  
 450 455 460  
 Ser Ile Gly Leu Gly Phe Ala Ile Pro Val Asp Gln Ala Lys Arg Ile  
 465 470 475 480  
 Ala Asp Glu Leu Ile Ser Thr Gly Lys Ala Ser His Ala Ser Leu Gly  
 485 490 495  
 Val Gln Val Thr Asn Asp Lys Asp Thr Pro Gly Ala Lys Ile Val Glu  
 500 505 510  
 Val Val Ala Gly Gly Ala Ala Ala Asn Ala Gly Val Pro Lys Gly Val  
 515 520 525  
 Val Val Thr Lys Val Asp Asp Arg Pro Ile Asn Ser Ala Asp Ala Leu  
 530 535 540  
 Val Ala Ala Val Arg Ser Lys Ala Pro Gly Ala Thr Val Ala Leu Thr  
 545 550 555 560  
 Phe Gln Asp Pro Ser Gly Gly Ser Arg Thr Val Gln Val Thr Leu Gly  
 565 570 575  
 Lys Ala Glu Gln  
 580

## (2) INFORMATION FOR SEQ ID NO:76:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Met Asn Asp Gly Lys Arg Ala Val Thr Ser Ala Val Leu Val Val Leu  
 1 5 10 15  
 Gly Ala Cys Leu Ala Leu Trp Leu Ser Gly Cys Ser Ser Pro Lys Pro  
 20 25 30  
 Asp Ala Glu Glu Gln Gly Val Pro Val Ser Pro Thr Ala Ser Asp Pro  
 35 40 45  
 Ala Leu Leu Ala Glu Ile Arg Gln Ser Leu Asp Ala Thr Lys Gly Leu  
 50 55 60  
 Thr Ser Val His Val Ala Val Arg Thr Thr Gly Lys Val Asp Ser Leu  
 65 70 75 80  
 Leu Gly Ile Thr Ser Ala Asp Val Asp Val Arg Ala Asn Pro Leu Ala  
 85 90 95  
 Ala Lys Gly Val Cys Thr Tyr Asn Asp Glu Gln Gly Val Pro Phe Arg  
 100 105 110  
 Val Gln Gly Asp Asn Ile Ser Val Lys Leu Phe Asp Asp Trp Ser Asn  
 115 120 125

Leu Gly Ser Ile Ser Glu Leu Ser Thr Ser Arg Val Leu Asp Pro Ala  
 130 135 140  
 Ala Gly Val Thr Gln Leu Leu Ser Gly Val Thr Asn Leu Gln Ala Gln  
 145 150 155 160  
 Gly Thr Glu Val Ile Asp Gly Ile Ser Thr Thr Lys Ile Thr Gly Thr  
 165 170 175  
 Ile Pro Ala Ser Ser Val Lys Met Leu Asp Pro Gly Ala Lys Ser Ala  
 180 185 190  
 Arg Pro Ala Thr Val Trp Ile Ala Gln Asp Gly Ser His His Leu Val  
 195 200 205  
 Arg Ala Ser Ile Asp Leu Gly Ser Gly Ser Ile Gln Leu Thr Gln Ser  
 210 215 220  
 Lys Trp Asn Glu Pro Val Asn Val Asp  
 225 230

## (2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 66 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Val Ile Asp Ile Ile Gly Thr Ser Pro Thr Ser Trp Glu Gln Ala Ala  
 1 5 10 15  
 Ala Glu Ala Val Gln Arg Ala Arg Asp Ser Val Asp Asp Ile Arg Val  
 20 25 30  
 Ala Arg Val Ile Glu Gln Asp Met Ala Val Asp Ser Ala Gly Lys Ile  
 35 40 45  
 Thr Tyr Arg Ile Lys Leu Glu Val Ser Phe Lys Met Arg Pro Ala Gln  
 50 55 60  
 Pro Arg  
 65

## (2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 69 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Val Pro Pro Ala Pro Pro Leu Pro Pro Leu Pro Pro Ser Pro Ile Ser  
 1 5 10 15



Cys Ala Ser Pro Pro Ser Pro Pro Leu Pro Pro Ala Pro Pro Val Ala  
                     20                    25                    30  
 Pro Gly Pro Pro Met Pro Pro Leu Asp Pro Trp Pro Pro Ala Pro Pro  
                     35                    40                    45  
 Leu Pro Tyr Ser Thr Pro Pro Gly Ala Pro Leu Pro Pro Ser Pro Pro  
                     50                    55                    60  
 Ser Pro Pro Leu Pro  
                     65

## (2) INFORMATION FOR SEQ ID NO:79:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Met Ser Asn Ser Arg Arg Arg Ser Leu Arg Trp Ser Trp Leu Leu Ser  
 1                    5                    10                    15  
 Val Leu Ala Ala Val Gly Leu Gly Leu Ala Thr Ala Pro Ala Gln Ala  
                     20                    25                    30  
 Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu  
                     35                    40                    45  
 Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val  
                     50                    55                    60  
 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr  
 65                    70                    75                    80  
 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val  
                     85                    90                    95  
 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln  
                     100                    105                    110  
 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala  
                     115                    120                    125  
 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly  
                     130                    135                    140  
 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly  
 145                    150                    155                    160  
 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu  
                     165                    170                    175  
 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr  
                     180                    185                    190  
 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser  
                     195                    200                    205

Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr  
 210 215 220  
 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala  
 225 230 235 240  
 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly  
 245 250 255  
 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu  
 260 265 270  
 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val  
 275 280 285  
 Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile  
 290 295 300  
 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp  
 305 310 315 320  
 Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp Gln  
 325 330 335  
 Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly  
 340 345 350  
 Pro Pro Ala  
 355

## (2) INFORMATION FOR SEQ ID NO:80:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Ser Pro Lys Pro Asp Ala Glu Glu Gln Gly Val Pro Val Ser Pro Thr  
 1 5 10 15  
 Ala Ser Asp Pro Ala Leu Leu Ala Glu Ile Arg Gln Ser Leu Asp Ala  
 20 25 30  
 Thr Lys Gly Leu Thr Ser Val His Val Ala Val Arg Thr Thr Gly Lys  
 35 40 45  
 Val Asp Ser Leu Leu Gly Ile Thr Ser Ala Asp Val Asp Val Arg Ala  
 50 55 60  
 Asn Pro Leu Ala Ala Lys Gly Val Cys Thr Tyr Asn Asp Glu Gln Gly  
 65 70 75 80  
 Val Pro Phe Arg Val Gln Gly Asp Asn Ile Ser Val Lys Leu Phe Asp  
 85 90 95  
 Asp Trp Ser Asn Leu Gly Ser Ile Ser Glu Leu Ser Thr Ser Arg Val  
 100 105 110

Leu Asp Pro Ala Ala Gly Val Thr Gln Leu Leu Ser Gly Val Thr Asn  
           115                                  120                                  125  
 Leu Gln Ala Gln Gly Thr Glu Val Ile Asp Gly Ile Ser Thr Thr Lys  
       130                                  135                                  140  
 Ile Thr Gly Thr Ile Pro Ala Ser Ser Val Lys Met Leu Asp Pro Gly  
 145                                  150                                  155                                  160  
 Ala Lys Ser Ala Arg Pro Ala Thr Val Trp Ile Ala Gln Asp Gly Ser  
                                   165                                  170                                  175  
 His His Leu Val Arg Ala Ser Ile Asp Leu Gly Ser Gly Ser Ile Gln  
                                   180                                  185                                  190  
 Leu Thr Gln Ser Lys Trp Asn Glu Pro Val Asn Val Asp  
       195                                  200                                  205

## (2) INFORMATION FOR SEQ ID NO:81:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Gly Asp Ser Phe Trp Ala Ala Ala Asp Gln Met Ala Arg Gly Phe Val  
 1                                  5                                  10                                  15  
 Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Gln  
                                   20                                  25                                  30  
 His Ala Asp Gly His Ser Leu Leu Leu Asp Ala Thr Asn Pro Ala Val  
       35                                  40                                  45  
 Val Ala Tyr Asp Pro Ala Phe Ala Tyr Glu Ile Gly Tyr Ile Xaa Glu  
       50                                  55                                  60  
 Ser Gly Leu Ala Arg Met Cys Gly Glu Asn Pro Glu Asn Ile Phe Phe  
 65                                  70                                  75                                  80  
 Tyr Ile Thr Val Tyr Asn Glu Pro Tyr Val Gln Pro Pro Glu Pro Glu  
                                   85                                  90                                  95  
 Asn Phe Asp Pro Glu Gly Val Leu Gly Gly Ile Tyr Arg Tyr His Ala  
                                   100                                  105                                  110  
 Ala Thr Glu Gln Arg Thr Asn Lys Xaa Gln Ile Leu Ala Ser Gly Val  
       115                                  120                                  125  
 Ala Met Pro Ala Ala Leu Arg Ala Ala Gln Met Leu Ala Ala Glu Trp  
       130                                  135                                  140  
 Asp Val Ala Ala Asp Val Trp Ser Val Thr Ser Trp Gly Glu Leu Asn  
 145                                  150                                  155                                  160  
 Arg Asp Gly Val Val Ile Glu Thr Glu Lys Leu Arg His Pro Asp Arg  
                                   165                                  170                                  175

Pro Ala Gly Val Pro Tyr Val Thr Arg Ala Leu Glu Asn Ala Arg Gly  
                     180                    185                    190

Pro Val Ile Ala Val Ser Asp Trp Met Arg Ala Val Pro Glu Gln Ile  
                     195                    200                    205

Arg Pro Trp Val Pro Gly Thr Tyr Leu Thr Leu Gly Thr Asp Gly Phe  
                     210                    215                    220

Gly Phe Ser Asp Thr Arg Pro Ala Gly Arg Arg Tyr Phe Asn Thr Asp  
                     225                    230                    235                    240

Ala Glu Ser Gln Val Gly Arg Gly Phe Gly Arg Gly Trp Pro Gly Arg  
                     245                    250                    255

Arg Val Asn Ile Asp Pro Phe Gly Ala Gly Arg Gly Pro Pro Ala Gln  
                     260                    265                    270

Leu Pro Gly Phe Asp Glu Gly Gly Gly Leu Arg Pro Xaa Lys  
                     275                    280                    285

## (2) INFORMATION FOR SEQ ID NO:82:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Thr Lys Phe His Ala Leu Met Gln Glu Gln Ile His Asn Glu Phe Thr  
   1                    5                    10                    15

Ala Ala Gln Gln Tyr Val Ala Ile Ala Val Tyr Phe Asp Ser Glu Asp  
                     20                    25                    30

Leu Pro Gln Leu Ala Lys His Phe Tyr Ser Gln Ala Val Glu Glu Arg  
                     35                    40                    45

Asn His Ala Met Met Leu Val Gln His Leu Leu Asp Arg Asp Leu Arg  
                     50                    55                    60

Val Glu Ile Pro Gly Val Asp Thr Val Arg Asn Gln Phe Asp Arg Pro  
                     65                    70                    75                    80

Arg Glu Ala Leu Ala Leu Ala Leu Asp Gln Glu Arg Thr Val Thr Asp  
                     85                    90                    95

Gln Val Gly Arg Leu Thr Ala Val Ala Arg Asp Glu Gly Asp Phe Leu  
                     100                    105                    110

Gly Glu Gln Phe Met Gln Trp Phe Leu Gln Glu Gln Ile Glu Glu Val  
                     115                    120                    125

Ala Leu Met Ala Thr Leu Val Arg Val Ala Asp Arg Ala Gly Ala Asn  
                     130                    135                    140

Leu Phe Glu Leu Glu Asn Phe Val Ala Arg Glu Val Asp Val Ala Pro  
                     145                    150                    155                    160

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

Arg	Ala	Asp	Glu	Arg	Lys	Asn	Thr	Thr	Met	Lys	Met	Val	Lys	Ser	Ile
1			5						10					15	
Ala	Ala	Gly	Leu	Thr	Ala	Ala	Ala	Ala	Ile	Gly	Ala	Ala	Ala	Ala	Gly
		20					25					30			
Val	Thr	Ser	Ile	Met	Ala	Gly	Gly	Pro	Val	Val	Tyr	Gln	Met	Gln	Pro
		35					40					45			
Val	Val	Phe	Gly	Ala	Pro	Leu	Pro	Leu	Asp	Pro	Xaa	Ser	Ala	Pro	Xaa
	50					55					60				
Val	Pro	Thr	Ala	Ala	Gln	Trp	Thr	Xaa	Leu	Leu	Asn	Xaa	Leu	Xaa	Asp
65					70					75					80
Pro	Asn	Val	Ser	Phe	Xaa	Asn	Lys	Gly	Ser	Leu	Val	Glu	Gly	Gly	Ile
				85					90					95	
Gly	Gly	Xaa	Glu	Gly	Xaa	Xaa	Arg	Arg	Xaa	Gln					
			100					105							

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

Val 1	Leu	Ser	Val 5	Pro	Val	Gly	Asp	Gly	Phe 10	Trp	Xaa	Arg	Val 15	Val	Asn
Pro	Leu	Gly	Gln 20	Pro	Ile	Asp	Gly	Arg 25	Gly	Asp	Val	Asp	Ser 30	Asp	Thr
Arg	Arg	Ala 35	Leu	Glu	Leu	Gln 40	Ala	Pro	Ser	Val	Val	Xaa 45	Arg	Gln	Gly
Val	Lys 50	Glu	Pro	Leu	Xaa	Thr 55	Gly	Ile	Lys	Ala	Ile 60	Asp	Ala	Met	Thr
Pro 65	Ile	Gly	Arg	Gly 70	Gln	Arg	Gln	Leu	Ile 75	Ile	Gly	Asp	Arg	Lys 80	Thr

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

Met Tyr Arg Phe Ala Cys Arg Thr Leu Met Leu Ala Ala Cys Ile Leu  
1 5 10 15

Ala Thr Gly Val Ala Gly Leu Gly Val Gly Ala Gln Ser Ala Ala Gln  
20 25 30

Thr Ala Pro Val Pro Asp Tyr Tyr Trp Cys Pro Gly Gln Pro Phe Asp  
                   35                  40                  45

Pro Ala Trp Gly Pro Asn Trp Asp Pro Tyr Thr Cys His Asp Asp Phe  
           50                  55                  60

His Arg Asp Ser Asp Gly Pro Asp His Ser Arg Asp Tyr Pro Gly Pro  
   65                  70                  75                  80

Ile Leu Glu Gly Pro Val Leu Asp Asp Pro Gly Ala Ala Pro Pro Pro  
                   85                  90                  95

Pro Ala Ala Gly Gly Gly Ala  
                   100

## (2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 88 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Val Gln Cys Arg Val Trp Leu Glu Ile Gln Trp Arg Gly Met Leu Gly  
   1                  5                  10                  15

Ala Asp Gln Ala Arg Ala Gly Gly Pro Ala Arg Ile Trp Arg Glu His  
           20                  25                  30

Ser Met Ala Ala Met Lys Pro Arg Thr Gly Asp Gly Pro Leu Glu Ala  
           35                  40                  45

Thr Lys Glu Gly Arg Gly Ile Val Met Arg Val Pro Leu Glu Gly Gly  
   50                  55                  60

Gly Arg Leu Val Val Glu Leu Thr Pro Asp Glu Ala Ala Ala Leu Gly  
   65                  70                  75                  80

Asp Glu Leu Lys Gly Val Thr Ser  
                   85

## (2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 95 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile  
   1                  5                  10                  15

Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly  
           20                  25                  30

Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala  
           35                          40                          45

Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu  
       50                          55                          60

Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg  
   65                          70                          75                          80

Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe  
                           85                          90                          95

## (2) INFORMATION FOR SEQ ID NO:89:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Met Thr Gln Ser Gln Thr Val Thr Val Asp Gln Gln Glu Ile Leu Asn  
   1                          5                          10                          15

Arg Ala Asn Glu Val Glu Ala Pro Met Ala Asp Pro Pro Thr Asp Val  
           20                          25                          30

Pro Ile Thr Pro Cys Glu Leu Thr Xaa Xaa Lys Asn Ala Ala Gln Gln  
       35                          40                          45

Xaa Val Leu Ser Ala Asp Asn Met Arg Glu Tyr Leu Ala Ala Gly Ala  
       50                          55                          60

Lys Glu Arg Gln Arg Leu Ala Thr Ser Leu Arg Asn Ala Ala Lys Xaa  
   65                          70                          75                          80

Tyr Gly Glu Val Asp Glu Glu Ala Ala Thr Ala Leu Asp Asn Asp Gly  
           85                          90                          95

Glu Gly Thr Val Gln Ala Glu Ser Ala Gly Ala Val Gly Gly Asp Ser  
           100                          105                          110

Ser Ala Glu Leu Thr Asp Thr Pro Arg Val Ala Thr Ala Gly Glu Pro  
       115                          120                          125

Asn Phe Met Asp Leu Lys Glu Ala Ala Arg Lys Leu Glu Thr Gly Asp  
   130                          135                          140

Gln Gly Ala Ser Leu Ala His Xaa Gly Asp Gly Trp Asn Thr Xaa Thr  
  145                          150                          155                          160

Leu Thr Leu Gln Gly Asp  
                           165



## (2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 5 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Arg Ala Glu Arg Met  
 1 5

## (2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 263 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala Ala  
 1 5 10 15

Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu Thr  
 20 25 30

Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile Leu  
 35 40 45

Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val Asn  
 50 55 60

Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met Phe  
 65 70 75 80

Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu Pro Phe  
 85 90 95

Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln Ala  
 100 105 110

Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu Met  
 115 120 125

Asn Asn Val Pro Gln Ala Leu Lys Gln Leu Ala Gln Pro Thr Gln Gly  
 130 135 140

Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser Pro  
 145 150 155 160

His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His Met  
 165 170 175

Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser Met  
 180 185 190

Leu Lys Gly Phe Ala Pro Ala Ala Ala Gln Ala Val Gln Thr Ala  
           195                                  200                                  205  
 Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu Gly  
           210                                  215                                  220  
 Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala Ala  
   225                                  230                                  235                                  240  
 Ser Val Arg Tyr Gly His Arg Asp Gly Gly Lys Tyr Ala Xaa Ser Gly  
                                   245                                  250                                  255  
 Arg Arg Asn Gly Gly Pro Ala  
                                   260

## (2) INFORMATION FOR SEQ ID NO:92:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Met Thr Tyr Ser Pro Gly Asn Pro Gly Tyr Pro Gln Ala Gln Pro Ala  
 1                                  5                                  10                                  15  
 Gly Ser Tyr Gly Gly Val Thr Pro Ser Phe Ala His Ala Asp Glu Gly  
           20                                  25                                  30  
 Ala Ser Lys Leu Pro Met Tyr Leu Asn Ile Ala Val Ala Val Leu Gly  
           35                                  40                                  45  
 Leu Ala Ala Tyr Phe Ala Ser Phe Gly Pro Met Phe Thr Leu Ser Thr  
           50                                  55                                  60  
 Glu Leu Gly Gly Gly Asp Gly Ala Val Ser Gly Asp Thr Gly Leu Pro  
 65                                  70                                  75                                  80  
 Val Gly Val Ala Leu Leu Ala Ala Leu Leu Ala Gly Val Val Leu Val  
                                   85                                  90                                  95  
 Pro Lys Ala Lys Ser His Val Thr Val Val Ala Val Leu Gly Val Leu  
                                   100                                  105                                  110  
 Gly Val Phe Leu Met Val Ser Ala Thr Phe Asn Lys Pro Ser Ala Tyr  
           115                                  120                                  125  
 Ser Thr Gly Trp Ala Leu Trp Val Val Leu Ala Phe Ile Val Phe Gln  
           130                                  135                                  140  
 Ala Val Ala Ala Val Leu Ala Leu Leu Val Glu Thr Gly Ala Ile Thr  
 145                                  150                                  155                                  160  
 Ala Pro Ala Pro Arg Pro Lys Phe Asp Pro Tyr Gly Gln Tyr Gly Arg  
                                   165                                  170                                  175  
 Tyr Gly Gln Tyr Gly Gln Tyr Gly Val Gln Pro Gly Gly Tyr Tyr Gly  
           180                                  185                                  190

Gln Gln Gly Ala Gln Gln Ala Ala Gly Leu Gln Ser Pro Gly Pro Gln  
           195                                  200                                  205  
 Gln Ser Pro Gln Pro Pro Gly Tyr Gly Ser Gln Tyr Gly Gly Tyr Ser  
           210                                  215                                  220  
 Ser Ser Pro Ser Gln Ser Gly Ser Gly Tyr Thr Ala Gln Pro Pro Ala  
   225                                  230                                  235                                  240  
 Gln Pro Pro Ala Gln Ser Gly Ser Gln Gln Ser His Gln Gly Pro Ser  
                                   245                                  250                                  255  
 Thr Pro Pro Thr Gly Phe Pro Ser Phe Ser Pro Pro Pro Pro Val Ser  
                                   260                                  265                                  270  
 Ala Gly Thr Gly Ser Gln Ala Gly Ser Ala Pro Val Asn Tyr Ser Asn  
           275                                  280                                  285  
 Pro Ser Gly Gly Glu Gln Ser Ser Ser Pro Gly Gly Ala Pro Val  
           290                                  295                                  300

## (2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Gly Cys Gly Glu Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly Asn  
 1                                  5                                  10                                  15  
 Phe Glu Arg Ile Ser Gly Asp Leu Lys Thr Gln Ile  
                                   20                                  25

## (2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Asp Gln Val Glu Ser Thr Ala Gly Ser Leu Gln Gly Gln Trp Arg Gly  
 1                                  5                                  10                                  15

## (2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Gly	Cys	Gly	Ser	Thr	Ala	Gly	Ser	Leu	Gln	Gly	Gln	Trp	Arg	Gly	Ala
1				5				10						15	
Ala	Gly	Thr	Ala	Ala	Gln	Ala	Ala	Val	Val	Arg					
			20					25							

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Gly	Cys	Gly	Gly	Thr	Ala	Ala	Gln	Ala	Ala	Val	Val	Arg	Phe	Gln	Glu
1				5				10						15	
Ala	Ala	Asn	Lys	Gln	Lys	Gln	Glu	Leu	Asp	Glu					
			20					25							

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Gly	Cys	Gly	Ala	Asn	Lys	Gln	Lys	Gln	Glu	Leu	Asp	Glu	Ile	Ser	Thr
1				5				10						15	
Asn	Ile	Arg	Gln	Ala	Gly	Val	Gln	Tyr	Ser	Arg					
			20					25							

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Gly	Cys	Gly	Ile	Arg	Gln	Ala	Gly	Val	Gln	Tyr	Ser	Arg	Ala	Asp	Glu
1				5				10						15	
Glu	Gln	Gln	Gln	Ala	Leu	Ser	Ser	Gln	Met	Gly	Phe				
			20					25							

## (2) INFORMATION FOR SEQ ID NO:99:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

```

ATGAAGATGG TGAAATCGAT CGCCGCAGGT CTGACCGCCG CGGCTGCAAT CGGCGCCGCT      60
GCGGCCGGTG TGAATTCGAT CATGGCTGGC GGCCCGGTCG TATACCAGAT GCAGCCGGTC      120
GTCTTCGGCG CGCCACTGCC GTTGGACCCG GCATCCGCCC CTGACGTCCC GACCGCCGCC      180
CAGTTGACCA GCCTGCTCAA CAGCCTCGCC GATCCCAACG TGTCGTTTGC GAACAAGGGC      240
AGTCTGGTCG AGGGCGGCAT CGGGGGCACC GAGGCGCGCA TCGCCGACCA CAAGCTGAAG      300
AAGGCCGCCG AGCACGGGGA TCTGCCGCTG TCGTTCAGCG TGACGAACAT CCAGCCGGCG      360
GCCGCCGGTT CGGCCACCGC CGACGTTTCC GTCTCGGGTC CGAAGCTCTC GTCGCCGGTC      420
ACGCAGAACG TCACGTTCGT GAATCAAGGC GGCTGGATGC TGTCACGCGC ATCGGCGATG      480
GAGTTGCTGC AGGCCGCAGG GAACTGA                                         507

```

## (2) INFORMATION FOR SEQ ID NO:100:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

```

Met Lys Met Val Lys Ser Ile Ala Ala Gly Leu Thr Ala Ala Ala Ala
1           5           10           15

Ile Gly Ala Ala Ala Ala Gly Val Thr Ser Ile Met Ala Gly Gly Pro
20          25          30

Val Val Tyr Gln Met Gln Pro Val Val Phe Gly Ala Pro Leu Pro Leu
35          40          45

Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln Leu Thr Ser
50          55          60

Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala Asn Lys Gly
65          70          75          80

Ser Leu Val Glu Gly Gly Ile Gly Gly Thr Glu Ala Arg Ile Ala Asp
85          90          95

His Lys Leu Lys Lys Ala Ala Glu His Gly Asp Leu Pro Leu Ser Phe
100         105         110

```

Ser Val Thr Asn Ile Gln Pro Ala Ala Ala Gly Ser Ala Thr Ala Asp  
 115 120 125

Val Ser Val Ser Gly Pro Lys Leu Ser Ser Pro Val Thr Gln Asn Val  
 130 135 140

Thr Phe Val Asn Gln Gly Gly Trp Met Leu Ser Arg Ala Ser Ala Met  
 145 150 155 160

Glu Leu Leu Gln Ala Ala Gly Asn  
 165

## (2) INFORMATION FOR SEQ ID NO:101:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

CGTGGCAATG TCGTTGACCG TCGGGGCCGG GGTGCCTCC GCAGATCCCG TGGACGCGGT	60
CATTAACACC ACCTGCAATT ACGGGCAGGT AGTAGCTGCG CTCAACGCGA CGGATCCGGG	120
GGCTGCCGCA CAGTTCAACG CCTCACCGGT GGCGCAGTCC TATTGCGCA ATTCCTCGC	180
CGCACCGCCA CCTCAGCGCG CTGCCATGGC CGCGCAATTG CAAGCTGTGC CGGGGGCGGC	240
ACAGTACATC GGCCTTGTCG AGTCGGTTGC CGGCTCCTGC AACAACTATT AAGCCCATGC	300
GGGCCCCATC CCGCGACCCG GCATCGTCGC CGGGGCTAGG CCAGATTGCC CCGCTCCTCA	360
ACGGGCCGCA TCCCGCGACC CGGCATCGTC GCCGGGGCTA GGCCAGATTG CCGCTCCT	420
CAACGGGCCG CATCTCGTGC CGAATTCCTG CAGCCCGGGG GATCCACTAG TTCTAGAGCG	480
GCCGCCACCG CGGTGGAGCT	500

## (2) INFORMATION FOR SEQ ID NO:102:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Val Ala Met Ser Leu Thr Val Gly Ala Gly Val Ala Ser Ala Asp Pro  
 1 5 10 15

Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val Val Ala  
 20 25 30

Ala Leu Asn Ala Thr Asp Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser  
 35 40 45

Pro Val Ala Gln Ser Tyr Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro  
 50 55 60

Gln Arg Ala Ala Met Ala Ala Gln Leu Gln Ala Val Pro Gly Ala Ala  
 65 70 75 80

Gln Tyr Ile Gly Leu Val Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr  
 85 90 95

## (2) INFORMATION FOR SEQ ID NO:103:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

ATGACAGAGC AGCAGTGGAA TTTCGCGGGT ATCGAGGCCG CGGCAAGCGC AATCCAGGGA 60

AATGTCACGT CCATTCATTC CCTCCTTGAC GAGGGGAAGC AGTCCCTGAC CAAGCTCGCA 120

GCGGCCTGGG GCGGTAGCGG TTCGGAAGCG TACC 154

## (2) INFORMATION FOR SEQ ID NO:104:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Met Thr Glu Gln Gln Trp Asn Phe Ala Gly Ile Glu Ala Ala Ala Ser  
 1 5 10 15

Ala Ile Gln Gly Asn Val Thr Ser Ile His Ser Leu Leu Asp Glu Gly  
 20 25 30

Lys Gln Ser Leu Thr Lys Leu Ala Ala Ala Trp Gly Gly Ser Gly Ser  
 35 40 45

Glu Ala Tyr  
 50

## (2) INFORMATION FOR SEQ ID NO:105:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CGGTCGCGCA CTTCCAGGTG ACTATGAAAG TCGGCTTCCG NCTGGAGGAT TCCTGAACCT 60

TCAAGCGCGG	CCGATAACTG	AGGTGCATCA	TTAAGCGACT	TTTCCAGAAC	ATCCTGACGC	120
GCTCGAAACG	CGGCACAGCC	GACGGTGGCT	CCGNCGAGGC	GCTGNCTCCA	AAATCCCTGA	180
GACAATTTCG	CGGGGGCGCC	TACAAGGAAG	TCGGTGCTGA	ATTCGNCGNG	TATCTGGTCG	240
ACCTGTGTGG	TCTGNAGCCG	GACGAAGCGG	TGCTCGACGT	CG		282

## (2) INFORMATION FOR SEQ ID NO:106:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GATCGTACCC	GTGCGAGTGC	TCGGGCCGTT	TGAGGATGGA	GTGCACGTGT	CTTTCGTGAT	60
GGCATAACCA	GAGATGTTGG	CGGCGGCGGC	TGACACCCTG	CAGAGCATCG	GTGCTACCAC	120
TGTGGCTAGC	AATGCCGCTG	CGGCGGCCCC	GACGACTGGG	GTGGTGCCCC	CCGCTGCCGA	180
TGAGGTGTCT	GCGCTGACTG	CGGCGCACTT	CGCCGCACAT	GCGGCGATGT	ATCAGTCCGT	240
GAGCGCTCGG	GCTGCTGCGA	TTCATGACCA	GTTTCGTGGC	ACCCTTGCCA	GCAGCGCCAG	300
CTCGTATGCG	GCCACTGAAG	TCGCCAATGC	GGCGGCGGCC	AGCTAAGCCA	GGAACAGTCG	360
GCACGAGAAA	CCACGAGAAA	TAGGGACACG	TAATGGTGGA	TTTCGGGGCG	TTACCACCGG	420
AGATCAACTC	CGCGAGGATG	TACGCCGGCC	CGGGTTCGGC	CTCGCTGGTG	GCCGCGGCTC	480
AGATGTGGGA	CAGCGTGGCG	AGTGACCTGT	TTTCGGCCGC	GTCGGCGTTT	CAGTCGGTGG	540
TCTGGGGTCT	GACGGTGGGG	TCGTGGATAG	GTTTCGTGGC	GGGTCTGATG	GTGGCGGCGG	600
CCTCGCCGTA	TGTGGCGTGG	ATGAGCGTCA	CCGCGGGGCA	GGCCGAGCTG	ACCGCCGCCC	660
AGGTCCGGGT	TGCTGCGGCG	GCCTACGAGA	CGGCGTATGG	GCTGACGGTG	CCCCCGCCGG	720
TGATCGCCGA	GAACCGTGCT	GAAGTATGA	TTCTGATAGC	GACCAACCTC	TTGGGGCAAA	780
ACACCCCGGC	GATCGCGGTC	AACGAGGCCG	AATACGGCGA	GATGTGGGCC	CAAGACGCCG	840
CCGCGATGTT	TGGCTACGCC	GCGGCGACGG	CGACGGCGAC	GGCGACGTTG	CTGCCGTTCT	900
AGGAGGCGCC	GGAGATGACC	AGCGCGGGTG	GGCTCCTCGA	GCAGGCCGCC	GCGGTCGAGG	960
AGGCCTCCGA	CACCGCCGCG	GCGAACCAGT	TGATGAACAA	TGTGCCCCAG	GCGCTGCAAC	1020
AGCTGGCCCA	GCCCACGCAG	GGCACCACGC	CTTCTTCCAA	GCTGGGTGGC	CTGTGGAAGA	1080
CGGTCTCGCC	GCATCGGTCG	CCGATCAGCA	ACATGGTGTC	GATGGCCAAC	AACCACATGT	1140
CGATGACCAA	CTCGGGTGTG	TCGATGACCA	ACACCTTGAG	CTCGATGTTG	AAGGGCTTTG	1200
CTCCGGCGGC	GGCCGCCCAG	GCCGTGCAAA	CCGCGGCGCA	AAACGGGGTC	CGGGCGATGA	1260



GCTCGCTGGG	CAGCTCGCTG	GGTTCTTCGG	GTCTGGGCGG	TGGGGTGGCC	GCCAACTTGG	1320
GTCGGGCGGC	CTCGGTCTGGT	TCGTTGTTCGG	TGCCGCAGGC	CTGGGCCGCG	GCCAACCAGG	1380
CAGTCACCCC	GGCGGCGCGG	GCGCTGCCGC	TGACCAGCCT	GACCAGCGCC	GCGGAAAGAG	1440
GGCCCGGGCA	GATGCTGGGC	GGGCTGCCGG	TGGGGCAGAT	GGGCGCCAGG	GCCGGTGGTG	1500
GGCTCAGTGG	TGTGCTGCGT	GTTCCGCCGC	GACCCTATGT	GATGCCGCAT	TCTCCGGCGG	1560
CCGGCTAGGA	GAGGGGGCGC	AGACTGTCGT	TATTTGACCA	GTGATCGGCG	GTCTCGGTGT	1620
TTCCGCGGCC	GGCTATGACA	ACAGTCAATG	TGCATGACAA	GTTACAGGTA	TTAGGTCCAG	1680
GTTCAACAAG	GAGACAGGCA	ACATGGCCTC	ACGTTTTATG	ACGGATCCGC	ACGCGATGCG	1740
GGACATGGCG	GGCCGTTTTG	AGGTGCACGC	CCAGACGGTG	GAGGACGAGG	CTCGCCGGAT	1800
GTGGGCGTCC	GCGCAAAACA	TTTCCGGTGC	GGGCTGGAGT	GGCATGGCCG	AGGCGACCTC	1860
GCTAGACACC	ATGGCCCAGA	TGAATCAGGC	GTTTCGCAAC	ATCGTGAACA	TGCTGCACGG	1920
GGTGCGTGAC	GGGCTGGTTC	GCGACGCCAA	CAACTACGAG	CAGCAAGAGC	AGGCCTCCCA	1980
GCAGATCCTC	AGCAGCTAAC	GTCAGCCGCT	GCAGACAAT	ACTTTTACAA	GCGAAGGAGA	2040
ACAGGTTCGA	TGACCATCAA	CTATCAATTC	GGGGATGTCT	ACGCTCACGG	CGCCATGATC	2100
CGCGCTCAGG	CCGGGTGCT	GGAGGCCGAG	CATCAGGCCA	TCATTCTGTA	TGTGTTGACC	2160
GCGAGTGACT	TTTGGGGCGG	CGCCGGTTTC	GCGGCCTGCC	AGGGGTTCAT	TACCCAGTTG	2220
GGCCGTAACT	TCCAGGTGAT	CTACGAGCAG	GCCAACGCCC	ACGGGCAGAA	GGTGCAGGCT	2280
GCCGGCAACA	ACATGGCGCA	AACCGACAGC	GCCGTCGGCT	CCAGCTGGGC	CTGACACCAG	2340
GCCAAGGCCA	GGGACGTGGT	GTACGAGTGA	AGTTCCTCGC	GTGATCCTTC	GGGTGGCAGT	2400
CTAAGTGATC	AGTGCTGGGG	TGTTGGTGGT	TTGCTGCTTG	GCGGGTTCTT	CGGTGCTGGT	2460
CAGTGCTGCT	CGGGCTCGGG	TGAGGACCTC	GAGGCCAGG	TAGCGCCGTC	CTTCGATCCA	2520
TTCGTCGTGT	TGTTCCGGCA	GGACGGCTCC	GACGAGGCGG	ATGATCGAGG	CGCGGTCGGG	2580
GAAGATGCCC	ACGACGTCGG	TTCGGCGTCG	TACCTCTCGG	TTGAGGCGTT	CCTGGGGGTT	2640
GTTGGACCAG	ATTTGGCGCC	AGATCTGCTT	GGGGAAGGCG	GTGAACGCCA	GCAGGTCGGT	2700
GCGGGCGGTG	TCGAGGTGCT	CGGCCACCGC	GGGGAGTTTG	TCGGTCAGAG	CGTCGAGTAC	2760
CCGATCATAT	TGGGCAACAA	CTGATTCCGG	GTCGGGCTGG	TCGTAGATGG	AGTGCAGCAG	2820
GGTGCGCACC	CACGGCCAGG	AGGGCTTCGG	GGTGGCTGCC	ATCAGATTGG	CTGCGTAGTG	2880
GGTTCTGCAG	CGCTGCCAGG	CCGCTGCGGG	CAGGGTGGCG	CCGATCGCGG	CCACCAGGCC	2940
GGCGTGGGCG	TCGCTGGTGA	CCAGCGCGAC	CCCGGACAGG	CCGCGGGCGA	CCAGGTCGCG	3000
GAAGAACGCC	AGCCAGCCGG	CCCCGTCCTC	GGCGGAGGTG	ACCTGGATGC	CCAGGATC	3058

## (2) INFORMATION FOR SEQ ID NO:107:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

```

Met Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
1           5           10           15

Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp
          20           25           30

Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
          35           40           45

Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
          50           55           60

Leu Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
65           70           75           80

Ala Gly Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
          85           90           95

Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala
          100          105          110

Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly
          115          120          125

Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met
          130          135          140

Trp Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala
145          150          155          160

Thr Ala Thr Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr
          165          170          175

Ser Ala Gly Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser
          180          185          190

Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu
          195          200          205

Gln Gln Leu Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu
          210          215          220

Gly Gly Leu Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn
225          230          235          240

Met Val Ser Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val
          245          250          255

Ser Met Thr Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala
          260          265          270

```

Ala Ala Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala  
 275 280 285

Met Ser Ser Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly  
 290 295 300

Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val  
 305 310 315 320

Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg  
 325 330 335

Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly  
 340 345 350

Gln Met Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly  
 355 360 365

Gly Gly Leu Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met  
 370 375 380

Pro His Ser Pro Ala Ala Gly  
 385 390

## (2) INFORMATION FOR SEQ ID NO:108:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1725 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GACGTCAGCA CCCGCCGTGC AGGGCTGGAG CGTGGTCGGT TTTGATCTGC GGTCAAGGTG	60
ACGTCCCTCG GCGTGTCGCC GGC GTGGATG CAGACTCGAT GCCGCTCTTT AGTGCAACTA	120
ATTTCTGTTGA AGTGCCTGCG AGGTATAGGA CTTACAGATT GGTAAATGTA GCGTTCACCC	180
CGTGTTGGGG TCGATTGGC CGGACCAGTC GTCACCAACG CTTGGCGTGC GCGCCAGGCG	240
GGCGATCAGA TCGCTTGACT ACCAATCAAT CTTGAGCTCC CGGGCCGATG CTCGGGCTAA	300
ATGAGGAGGA GCACGCGTGT CTTTCACTGC GCAACCGGAG ATGTTGGCGG CCGCGGCTGG	360
CGAACTTCGT TCCCTGGGGG CAACGCTGAA GGCTAGCAAT GCCGCCGAG CCGTGCCGAC	420
GACTGGGGTG GTGCCCCCGG CTGCCGACGA GGTGTCGCTG CTGCTTGCCA CACAATTCCG	480
TACGCATGCG GCGACGTATC AGACGGCCAG CGCCAAGGCC GCGGTGATCC ATGAGCAGTT	540
TGTGACCACG CTGGCCACCA GCGCTAGTTC ATATGCGGAC ACCGAGGCCG CCAACGCTGT	600
GGTCACCGGC TAGCTGACCT GACGGTATTC GAGCGGAAGG ATTATCGAAG TGGTGGATTT	660
CGGGGCGTTA CCACCGGAGA TCAACTCCGC GAGGATGTAC GCCGGCCCCG GTTCGGCCTC	720
GCTGGTGGCC GCCGCGAAGA TGTGGGACAG CGTGGCGAGT GACCTGTTTT CGGCCGCGTC	780

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GGCGTTTCAG TCGGTGGTCT GGGGTCTGAC GGTGGGGTCG TGGATAGGTT CGTCGGCGGG      840
TCTGATGGCG GCGGCGGCCT CGCCGTATGT GGC GTGGATG AGCGTCACCG CGGGGCAGGC      900
CCAGCTGACC GCCGCCCAGG TCCGGGTTGC TGCGGCGGCC TACGAGACAG CGTATAGGCT      960
GACGGTGCCC CCGCCGGTGA TCGCCGAGAA CCGTACCGAA CTGATGACGC TGACCGCGAC     1020
CAACCTCTTG GGGCAAAACA CGCCGGCGAT CGAGGCCAAT CAGGCCGCAT ACAGCCAGAT     1080
GTGGGGCCAA GACGCGGAGG CGATGTATGG CTACGCCGCC ACGGCGGCGA CGGCGACCGA     1140
GGCGTTGCTG CCGTTCGAGG ACGCCCCACT GATCACCAAC CCCGGCGGGC TCCTTGAGCA     1200
GGCCGTCGCG GTCGAGGAGG CCATCGACAC CGCCGCGGCG AACCAGTTGA TGAACAATGT     1260
GCCCCAAGCG CTGCAACAGC TGGCCCAGCC AGCGCAGGGC GTCGTACCTT CTTCCAAGCT     1320
GGGTGGGCTG TGGACGGCGG TCTCGCCGCA TCTGTGCGCG CTCAGCAACG TCAGTTCGAT     1380
AGCCAACAAC CACATGTCGA TGATGGGCAC GGGTGTGTGCG ATGACCAACA CCTTGCACTC     1440
GATGTTGAAG GGCTTAGCTC CGGCGGCGGC TCAGGCCGTG GAAACCGCGG CGGAAAACGG     1500
GGTCTGGGCG ATGAGCTCGC TGGGCAGCCA GCTGGGTTGCG TCGCTGGGTT CTTCGGGTCT     1560
GGGCGCTGGG GTGGCCGCCA ACTTGGGTGCG GGCGGCCTCG GTCGGTTCGT TGTCGGTGCC     1620
GCCAGCATGG GCCGCGGCCA ACCAGGCGGT CACCCCGGCG GCGCGGGCGC TGCCGCTGAC     1680
CAGCCTGACC AGCGCCGCCC AAACCGCCCC CGGACACATG CTGGG                      1725

```

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

```

Val Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
1           5           10           15
Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Lys Met Trp
20        25        30
Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
35        40        45
Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
50        55        60
Leu Met Ala Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
65        70        75        80
Ala Gly Gln Ala Gln Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
85        90        95

```

Ala	Tyr	Glu	Thr	Ala	Tyr	Arg	Leu	Thr	Val	Pro	Pro	Pro	Val	Ile	Ala	100	105	110
Glu	Asn	Arg	Thr	Glu	Leu	Met	Thr	Leu	Thr	Ala	Thr	Asn	Leu	Leu	Gly	115	120	125
Gln	Asn	Thr	Pro	Ala	Ile	Glu	Ala	Asn	Gln	Ala	Ala	Tyr	Ser	Gln	Met	130	135	140
Trp	Gly	Gln	Asp	Ala	Glu	Ala	Met	Tyr	Gly	Tyr	Ala	Ala	Thr	Ala	Ala	145	150	155
Thr	Ala	Thr	Glu	Ala	Leu	Leu	Pro	Phe	Glu	Asp	Ala	Pro	Leu	Ile	Thr	165	170	175
Asn	Pro	Gly	Gly	Leu	Leu	Glu	Gln	Ala	Val	Ala	Val	Glu	Glu	Ala	Ile	180	185	190
Asp	Thr	Ala	Ala	Ala	Asn	Gln	Leu	Met	Asn	Asn	Val	Pro	Gln	Ala	Leu	195	200	205
Gln	Gln	Leu	Ala	Gln	Pro	Ala	Gln	Gly	Val	Val	Pro	Ser	Ser	Lys	Leu	210	215	220
Gly	Gly	Leu	Trp	Thr	Ala	Val	Ser	Pro	His	Leu	Ser	Pro	Leu	Ser	Asn	225	230	235
Val	Ser	Ser	Ile	Ala	Asn	Asn	His	Met	Ser	Met	Met	Gly	Thr	Gly	Val	245	250	255
Ser	Met	Thr	Asn	Thr	Leu	His	Ser	Met	Leu	Lys	Gly	Leu	Ala	Pro	Ala	260	265	270
Ala	Ala	Gln	Ala	Val	Glu	Thr	Ala	Ala	Glu	Asn	Gly	Val	Trp	Ala	Met	275	280	285
Ser	Ser	Leu	Gly	Ser	Gln	Leu	Gly	Ser	Ser	Leu	Gly	Ser	Ser	Gly	Leu	290	295	300
Gly	Ala	Gly	Val	Ala	Ala	Asn	Leu	Gly	Arg	Ala	Ala	Ser	Val	Gly	Ser	305	310	315
Leu	Ser	Val	Pro	Pro	Ala	Trp	Ala	Ala	Ala	Asn	Gln	Ala	Val	Thr	Pro	325	330	335
Ala	Ala	Arg	Ala	Leu	Pro	Leu	Thr	Ser	Leu	Thr	Ser	Ala	Ala	Gln	Thr	340	345	350
Ala	Pro	Gly	His	Met	Leu	Gly										355		

## (2) INFORMATION FOR SEQ ID NO:110:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3027 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

AGTTCAGTCG	AGAATGATAC	TGACGGGCTG	TATCCACGAT	GGCTGAGACA	ACCGAACCAC	60
CGTCGGACGC	GGGGACATCG	CAAGCCGACG	CGATGGCGTT	GGCCGCCGAA	GCCGAAGCCG	120
CCGAAGCCGA	AGCGCTGGCC	GCCGCGGCGC	GGGCCCCTGC	CCGTGCCGCC	CGGTTGAAGC	180
GTGAGGCGCT	GGCGATGGCC	CCAGCCGAGG	ACGAGAACGT	CCCCGAGGAT	ATGCAGACTG	240
GGAAGACGCC	GAAGACTATG	ACGACTATGA	CGACTATGAG	GCCGCAGACC	AGGAGGCCGC	300
ACGGTCGGCA	TCCTGGCGAC	GGCGGTTGCG	GGTGCGGTTA	CCAAGACTGT	CCACGATTGC	360
CATGGCGGCC	GCAGTCGTCA	TCATCTGCGG	CTTCACCGGG	CTCAGCGGAT	ACATTGTGTG	420
GCAACACCAT	GAGGCCACCG	AACGCCAGCA	GCGCGCCGCG	GCGTTCGCCC	CCGGAGCCAA	480
GCAAGGTGTC	ATCAACATGA	CCTCGCTGGA	CTTCAACAAG	GCCAAAGAAG	ACGTCGCGCG	540
TGTGATCGAC	AGCTCCACCG	GCGAATTCAG	GGATGACTTC	CAGCAGCGGG	CAGCCGATTT	600
CACCAAGGTT	GTCGAACAGT	CCAAAGTGGT	CACCGAAGGC	ACGGTGAACG	CGACAGCCGT	660
CGAATCCATG	AACGAGCATT	CCGCCGTGGT	GCTCGTCGCG	GCGACTTCAC	GGGTCACCAA	720
TTCCGCTGGG	GCGAAAGACG	AACCACGTGC	GTGGCGGCTC	AAAGTGACCG	TGACCGAAGA	780
GGGGGGACAG	TACAAGATGT	CGAAAGTTGA	GTTTCGTACCG	TGACCGATGA	CGTACGCGAC	840
GTCAACACCG	AAACCACTGA	CGCCACCGAA	GTCGCTGAGA	TCGACTCAGC	CGCAGGCGAA	900
GCCGGTGATT	CGGCGACCGA	GGCATTGAC	ACCGACTCTG	CAACGGAATC	TACCGCGCAG	960
AAGGGTCAGC	GGCACCGTGA	CCTGTGGCGA	ATGCAGGTTA	CCTTGAAACC	CGTTCCGGTG	1020
ATTCTCATCC	TGCTCATGTT	GATCTCTGGG	GGCGCGACGG	GATGGCTATA	CCTTGAGCAA	1080
TACGACCCGA	TCAGCAGACG	GACTCCGGCG	CCGCCCCTGC	TGCCGTCGCC	GCGGCGTCTG	1140
ACGGGACAAT	CGCGCTGTTG	TGTATTCACC	CGACACGTGC	ACCAAGACTT	CGCTACCGCC	1200
AGGTGCGACC	TCGCCGGCGA	TTTCCTGTCC	TATACGACCA	G TTCACGCAG	CAGATCGTGG	1260
CTCCGGCGGC	CAAACAGAAG	TCACTGAAAA	CCACCGCCAA	GGTGGTGCGC	GCGGCCGTGT	1320
CGGAGCTACA	TCCGATTTCG	GCCGTCGTTC	TGGTTTTTGT	CGACCAGAGC	ACTACCAGTA	1380
AGGACAGCCC	CAATCCGTCG	ATGGCGGCCA	GCAGCGTGAT	GGTGACCCTA	GCCAAGGTCTG	1440
ACGGCAATTG	GCTGATCACC	AAGTTCACCC	CGGTTTAGGT	TGCCGTAGGC	GGTCGCCAAG	1500
TCTGACGGGG	GCGCGGGTGG	CTGCTCGTGC	GAGATACCGG	CCGTTCTCCG	GACAATCACG	1560
GCCCCACCTC	AAACAGATCT	CGGCCGCTGT	CTAATCGGCC	GGGTTATTTA	AGATTAGTTG	1620
CCACTGTATT	TACCTGATGT	TCAGATTGTT	CAGCTGGATT	TAGCTTCGCG	GCAGGGCGGC	1680
TGGTGCACTT	TGCATCTGGG	GTTGTGACTA	CTTGAGAGAA	TTTGACCTGT	TGCCGACGTT	1740
GTTTGCTGTC	CATCATTTGGT	GCTAGTTATG	GCCGAGCGGA	AGGATTATCG	AAGTGGTGGA	1800

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CTTCGGGGCG TTACCACCGG AGATCAACTC CGCGAGGATG TACGCCGGCC CGGGTTCGGC 1860
CTCGCTGGTG GCCGCCGCGA AGATGTGGGA CAGCGTGGCG AGTGACCTGT TTTCGGCCGC 1920
GTCGGCGTTT CAGTCGGTGG TCTGGGGTCT GACGACGGGA TCGTGGATAG GTTCGTTCGGC 1980
GGGTCTGATG GTGGCGGCGG CCTCGCCGTA TGTGGCGTGG ATGAGCGTCA CCGCGGGGCA 2040
GGCCGAGCTG ACCGCCGCCG AGGTCCGGGT TGCTGCGGCG GCCTACGAGA CGGCGTATGG 2100
GCTGACGGTG CCCCCGCCG TGATCGCCGA GAACCGTGCT GAACTGATGA TTCTGATAGC 2160
GACCAACCTC TTGGGGCAAA ACACCCCGGC GATCGCGGTC AACGAGGCCG AATACGGGGA 2220
GATGTGGGCC CAAGACGCCG CCGCGATGTT TGGCTACGCC GCCACGGCGG CGACGGCGAC 2280
CGAGGCGTTG CTGCCGTTCT AGGACGCCCC ACTGATCACC AACCCCGGCG GGCTCCTTGA 2340
GCAGGCCGTC GCGGTCGAGG AGGCCATCGA CACCGCCGCG GCGAACCAGT TGATGAACAA 2400
TGTGCCCCAA GCGCTGCAAC AACTGGCCCA GCCCACGAAA AGCATCTGGC CGTTCGACCA 2460
ACTGAGTGAA CTCTGGAAAG CCATCTCGCC GCATCTGTGC CCGCTCAGCA ACATCGTGTC 2520
GATGCTCAAC AACCACGTGT CGATGACCAA CTCGGGTGTG TCGATGGCCA GCACCTTGCA 2580
CTCAATGTTG AAGGGCTTTG CTCCGGCGGC GGCTCAGGCC GTGGAAACCG CGGCGCAAAA 2640
CGGGGTCCAG GCGATGAGCT CGCTGGGCAG CCAGCTGGGT TCGTCGCTGG GTTCTTCGGG 2700
TCTGGGCGCT GGGGTGGCCG CCAACTTGGG TCGGGCGGCC TCGGTCGGTT CGTTGTCGGT 2760
GCCGAGGCC TGGGCCGCGG CCAACCAGGC GGTACCCCCG GCGGCGCGGG CGCTGCCGCT 2820
GACCAGCCTG ACCAGCGCCG CCCAAACCGC CCCCAGACAC ATGCTGGGCG GGCTACCGCT 2880
GGGGCAACTG ACCAATAGCG GCGGCGGGTT CGGCGGGGTT AGCAATGCGT TCGGGATGCC 2940
GCCGCGGGCG TACGTAATGC CCCGTGTGCC CGCCGCCGGG TAACGCCGAT CCGCACGCAA 3000
TGCGGGCCCT CTATGCGGGC AGCGATC 3027

```

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

```

Val Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
1           5           10           15

Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Lys Met Trp
20           25           30

Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
35           40           45

```

Val	Val	Trp	Gly	Leu	Thr	Thr	Gly	Ser	Trp	Ile	Gly	Ser	Ser	Ala	Gly	50	55	60
Leu	Met	Val	Ala	Ala	Ala	Ser	Pro	Tyr	Val	Ala	Trp	Met	Ser	Val	Thr	65	70	75
Ala	Gly	Gln	Ala	Glu	Leu	Thr	Ala	Ala	Gln	Val	Arg	Val	Ala	Ala	Ala	85	90	95
Ala	Tyr	Glu	Thr	Ala	Tyr	Gly	Leu	Thr	Val	Pro	Pro	Pro	Val	Ile	Ala	100	105	110
Glu	Asn	Arg	Ala	Glu	Leu	Met	Ile	Leu	Ile	Ala	Thr	Asn	Leu	Leu	Gly	115	120	125
Gln	Asn	Thr	Pro	Ala	Ile	Ala	Val	Asn	Glu	Ala	Glu	Tyr	Gly	Glu	Met	130	135	140
Trp	Ala	Gln	Asp	Ala	Ala	Ala	Met	Phe	Gly	Tyr	Ala	Ala	Thr	Ala	Ala	145	150	155
Thr	Ala	Thr	Glu	Ala	Leu	Leu	Pro	Phe	Glu	Asp	Ala	Pro	Leu	Ile	Thr	165	170	175
Asn	Pro	Gly	Gly	Leu	Leu	Glu	Gln	Ala	Val	Ala	Val	Glu	Glu	Ala	Ile	180	185	190
Asp	Thr	Ala	Ala	Ala	Asn	Gln	Leu	Met	Asn	Asn	Val	Pro	Gln	Ala	Leu	195	200	205
Gln	Gln	Leu	Ala	Gln	Pro	Thr	Lys	Ser	Ile	Trp	Pro	Phe	Asp	Gln	Leu	210	215	220
Ser	Glu	Leu	Trp	Lys	Ala	Ile	Ser	Pro	His	Leu	Ser	Pro	Leu	Ser	Asn	225	230	235
Ile	Val	Ser	Met	Leu	Asn	Asn	His	Val	Ser	Met	Thr	Asn	Ser	Gly	Val	245	250	255
Ser	Met	Ala	Ser	Thr	Leu	His	Ser	Met	Leu	Lys	Gly	Phe	Ala	Pro	Ala	260	265	270
Ala	Ala	Gln	Ala	Val	Glu	Thr	Ala	Ala	Gln	Asn	Gly	Val	Gln	Ala	Met	275	280	285
Ser	Ser	Leu	Gly	Ser	Gln	Leu	Gly	Ser	Ser	Leu	Gly	Ser	Ser	Gly	Leu	290	295	300
Gly	Ala	Gly	Val	Ala	Ala	Asn	Leu	Gly	Arg	Ala	Ala	Ser	Val	Gly	Ser	305	310	315
Leu	Ser	Val	Pro	Gln	Ala	Trp	Ala	Ala	Ala	Asn	Gln	Ala	Val	Thr	Pro	325	330	335
Ala	Ala	Arg	Ala	Leu	Pro	Leu	Thr	Ser	Leu	Thr	Ser	Ala	Ala	Gln	Thr	340	345	350
Ala	Pro	Gly	His	Met	Leu	Gly	Gly	Leu	Pro	Leu	Gly	Gln	Leu	Thr	Asn	355	360	365



Ser Gly Gly Gly Phe Gly Gly Val Ser Asn Ala Leu Arg Met Pro Pro  
 370 375 380

Arg Ala Tyr Val Met Pro Arg Val Pro Ala Ala Gly  
 385 390 395

## (2) INFORMATION FOR SEQ ID NO:112:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CATCGGAGGG AGTGATCACC ATGCTGTGGC ACGCAATGCC ACCGGAGTAA ATACCGCACG	60
GCTGATGGCC GCGCGGGTC CGGCTCCAAT GCTTGCGGCG GCCGCGGGAT GGCAGACGCT	120
TTCGGCGGCT CTGGACGCTC AGGCCGTCGA GTTGACCGCG CGCCTGAACT CTCTGGGAGA	180
AGCCTGGACT GGAGGTGGCA GCGACAAGGC GCTTGCGGCT GCAACGCCGA TGGTGGTCTG	240
GCTACAAACC GCGTCAACAC AGGCCAAGAC CCGTGCGATG CAGGCGACGG CGCAAGCCGC	300
GGCATAACACC CAGGCCATGG CCACGACGCC GTCGCTGCCG GAGATCGCCG CCAACCACAT	360
CACCCAGGCC GTCCTTACGG CCACCAACTT CTTCGGTATC AACACGATCC CGATCGCGTT	420
GACCGAGATG GATTATTTCA TCCGTATGTG GAACCAGGCA GCCCTGGCAA TGGAGGTCTA	480
CCAGGCCGAG ACCGCGGTTA ACACGCTTTT CGAGAAGCTC GAGCCGATGG CGTCGATCCT	540
TGATCCCGGC GCGAGCCAGA GCACGACGAA CCCGATCTTC GGAATGCCCT CCCCTGGCAG	600
CTCAACACCG GTTGCCAGT TGCCGCCGGC GGCTACCCAG ACCCTCGGCC AACTGGGTGA	660
GATGAGCGGC CCGATGCAGC AGCTGACCCA GCCGCTGCAG CAGGTGACGT CGTTGTTCAG	720
CCAGGTGGGC GGCACCGGC GCGGCAACCC AGCCGACGAG GAAGCCGCGC AGATGGGCCT	780
GCTCGGCACC AGTCCGCTGT CGAACCATCC GCTGGCTGGT GGATCAGGCC CCAGCGCGGG	840
CGCGGGCCTG CTGCGCGCG AGTCGCTACC TGGCGCAGGT GGGTCGTTGA CCCGCACGCC	900
GCTGATGTCT CAGCTGATCG AAAAGCCGGT TGCCCCCTCG GTGATGCCGG CGGCTGCTGC	960
CGGATCGTCG GCGACGGGTG GCGCCGCTCC GGTGGGTGCG GGAGCGATGG GCCAGGGTGC	1020
GCAATCCGGC GGCTCCACCA GGCCGGGTCT GGTGCGGCCG GCACCGCTCG CGCAGGAGCG	1080
TGAAGAAGAC GACGAGGACG ACTGGGACGA AGAGGACGAC TGGTGAGCTC CCGTAATGAC	1140
AACAGACTTC CCGGCCACCC GGGCCGGAAG ACTTGCCAAC ATTTTGCGCA GGAAGGTAAA	1200
GAGAGAAAAGT AGTCCAGCAT GGCAGAGATG AAGACCGATG CCGCTACCCT CGCGCAGGAG	1260
GCAGGTAATT TCGAGCGGAT CTCCGGCGAC CTGAAAACCC AGATCGACCA GGTGGAGTCG	1320

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ACGGCAGGTT CGTTGCAGGG CCAGTGGCGC GGCGCGGCGG GGACGGCCGC CCAGGCCGCG      1380
GTGGTGCGCT TCCAAGAAGC AGCCAATAAG CAGAAGCAGG AACTCGACGA GATCTCGACG      1440
AATATTCGTC AGGCCGCGCT CCAATACTCG AGGGCCGACG AGGAGCAGCA GCAGGCGCTG      1500
TCCTCGCAAA TGGGCTTCTG ACCCGCTAAT ACGAAAAGAA ACGGAGCAAA AACATGACAG      1560
AGCAGCAGTG GAATTTTCGCG GGTATCGAGG CCGCGGCAAG CGCAATCCAG GGAAAT      1616

```

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 432 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

```

CTAGTGGATG GGACCATGGC CATTTTCTGC AGTCTCACTG CCTTCTGTGT TGACATTTTG      60
GCACGCCGGC GGAAACGAAG CACTGGGGTC GAAGAACGGC TGCGCTGCCA TATCGTCCGG      120
AGCTTCCATA CCTTCGTGCG GCCGGAAGAG CTTGTCTAG TCGGCCGCCA TGACAACCTC      180
TCAGAGTGCG CTCAAACGTA TAAACACGAG AAAGGGCGAG ACCGACGGAA GGTCGAACTC      240
GCCCCGATCCC GTGTTTCGCT ATTCTACGCG AACTCGGCGT TGCCCTATGC GAACATCCCA      300
GTGACGTTGC CTTCCGGTCGA AGCCATTGCC TGACCGGCTT CGCTGATCGT CCGCGCCAGG      360
TTCTGCAGCG CGTTGTTTCTG CTCGGTAGCC GTGGCGTCCC ATTTTGTCTG GACACCCTGG      420
TACGCCTCCG AA      432

```

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 368 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

```

Met Leu Trp His Ala Met Pro Pro Glu Xaa Asn Thr Ala Arg Leu Met
1           5           10           15
Ala Gly Ala Gly Pro Ala Pro Met Leu Ala Ala Ala Ala Gly Trp Gln
20           25           30
Thr Leu Ser Ala Ala Leu Asp Ala Gln Ala Val Glu Leu Thr Ala Arg
35           40           45
Leu Asn Ser Leu Gly Glu Ala Trp Thr Gly Gly Gly Ser Asp Lys Ala
50           55           60

```

Leu	Ala	Ala	Ala	Thr	Pro	Met	Val	Val	Trp	Leu	Gln	Thr	Ala	Ser	Thr	65	70	75	80
Gln	Ala	Lys	Thr	Arg	Ala	Met	Gln	Ala	Thr	Ala	Gln	Ala	Ala	Ala	Tyr	85	90	95	
Thr	Gln	Ala	Met	Ala	Thr	Thr	Pro	Ser	Leu	Pro	Glu	Ile	Ala	Ala	Asn	100	105	110	
His	Ile	Thr	Gln	Ala	Val	Leu	Thr	Ala	Thr	Asn	Phe	Phe	Gly	Ile	Asn	115	120	125	
Thr	Ile	Pro	Ile	Ala	Leu	Thr	Glu	Met	Asp	Tyr	Phe	Ile	Arg	Met	Trp	130	135	140	
Asn	Gln	Ala	Ala	Leu	Ala	Met	Glu	Val	Tyr	Gln	Ala	Glu	Thr	Ala	Val	145	150	155	160
Asn	Thr	Leu	Phe	Glu	Lys	Leu	Glu	Pro	Met	Ala	Ser	Ile	Leu	Asp	Pro	165	170	175	
Gly	Ala	Ser	Gln	Ser	Thr	Thr	Asn	Pro	Ile	Phe	Gly	Met	Pro	Ser	Pro	180	185	190	
Gly	Ser	Ser	Thr	Pro	Val	Gly	Gln	Leu	Pro	Pro	Ala	Ala	Thr	Gln	Thr	195	200	205	
Leu	Gly	Gln	Leu	Gly	Glu	Met	Ser	Gly	Pro	Met	Gln	Gln	Leu	Thr	Gln	210	215	220	
Pro	Leu	Gln	Gln	Val	Thr	Ser	Leu	Phe	Ser	Gln	Val	Gly	Gly	Thr	Gly	225	230	235	240
Gly	Gly	Asn	Pro	Ala	Asp	Glu	Glu	Ala	Ala	Gln	Met	Gly	Leu	Leu	Gly	245	250	255	
Thr	Ser	Pro	Leu	Ser	Asn	His	Pro	Leu	Ala	Gly	Gly	Ser	Gly	Pro	Ser	260	265	270	
Ala	Gly	Ala	Gly	Leu	Leu	Arg	Ala	Glu	Ser	Leu	Pro	Gly	Ala	Gly	Gly	275	280	285	
Ser	Leu	Thr	Arg	Thr	Pro	Leu	Met	Ser	Gln	Leu	Ile	Glu	Lys	Pro	Val	290	295	300	
Ala	Pro	Ser	Val	Met	Pro	Ala	Ala	Ala	Ala	Gly	Ser	Ser	Ala	Thr	Gly	305	310	315	320
Gly	Ala	Ala	Pro	Val	Gly	Ala	Gly	Ala	Met	Gly	Gln	Gly	Ala	Gln	Ser	325	330	335	
Gly	Gly	Ser	Thr	Arg	Pro	Gly	Leu	Val	Ala	Pro	Ala	Pro	Leu	Ala	Gln	340	345	350	
Glu	Arg	Glu	Glu	Asp	Asp	Glu	Asp	Asp	Trp	Asp	Glu	Glu	Asp	Asp	Trp	355	360	365	

## (2) INFORMATION FOR SEQ ID NO:115:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

```

Met Ala Glu Met Lys Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly
1           5           10           15
Asn Phe Glu Arg Ile Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val
          20           25           30
Glu Ser Thr Ala Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly
          35           40           45
Thr Ala Ala Gln Ala Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys
          50           55           60
Gln Lys Gln Glu Leu Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly
65           70           75           80
Val Gln Tyr Ser Arg Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser
          85           90           95
Gln Met Gly Phe
          100

```

## (2) INFORMATION FOR SEQ ID NO:116:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

```

GATCTCCGGC GACCTGAAAA CCCAGATCGA CCAGGTGGAG TCGACGGCAG GTTCGTTGCA      60
GGGCCAGTGG CGCGGCGCGG CGGGGACGGC CGCCCAGGCC GCGGTGGTGC GCTTCCAAGA      120
AGCAGCCAAT AAGCAGAAGC AGGAACTCGA CGAGATCTCG ACGAATATTC GTCAGGCCGG      180
CGTCCAATAC TCGAGGGCCG ACGAGGAGCA GCAGCAGGCG CTGTCCTCGC AAATGGGCTT      240
CTGACCCGCT AATACGAAAA GAAACGGAGC AAAAACATGA CAGAGCAGCA GTGGAATTTT      300
GCGGGTATCG AGGCCGCGGC AAGCGCAATC CAGGGAAATG TCACGTCCAT TCATTCCCTC      360
CTTGACGAGG GGAAGCAGTC CCTGACCAAG CTCGCA      396

```

## (2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 80 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

```

Ile Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala
1           5           10           15
Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln
20           25           30
Ala Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu
35           40           45
Leu Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser
50           55           60
Arg Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
65           70           75           80

```

## (2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 387 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

```

GTGGATCCCG ATCCCGTGTT TCGCTATTCT ACGCGAACTC GCGGTTGCCC TATGCGAACA      60
TCCCAGTGAC GTTGCCCTTCG GTCGAAGCCA TTGCCTGACC GGCTTCGCTG ATCGTCCGCG      120
CCAGGTTCTG CAGCGCGTTG TTCAGCTCGG TAGCCGTGGC GTCCCATTTT TGCTGGACAC      180
CCTGGTACGC CTCCGAACCG CTACCGCCCC AGGCCGCTGC GAGCTTGGTC AGGGACTGCT      240
TCCCCTCGTC AAGGAGGGAA TGAATGGACG TGACATTTCC CTGGATTGCG CTTGCCGCGG      300
CCTCGATACC CGCGAAATTC CACTGCTGCT CTGTCATGTT TTTGCTCCGT TTCTTTTCGT      360
ATTAGCGGGT CAGAAGCCCA TTTGCGA                                     387

```

## (2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 272 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

```

CGGCACGAGG ATCTCGGTTG GCCCAACGGC GCTGGCGAGG GCTCCGTTCC GGGGGCGAGC      60
TGCGCGCCGG ATGCTTCCTC TGCCCGCAGC CGCGCCTGGA TGGATGGACC AGTTGCTACC      120
TTCCCGACGT TTCGTTCGGT GTCTGTGCGA TAGCGGTGAC CCCGGCGCGC ACGTCGGGAG      180
TGTTGGGGGG CAGGCCGGGT CGGTGGTTCG GCCGGGGACG CAGACGGTCT GGACGGAACG      240
GGCGGGGGTT CGCCGATTGG CATCTTTGCC CA                                     272

```

## (2) INFORMATION FOR SEQ ID NO:120:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

```

Asp Pro Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val
1           5           10           15

Val Ala Ala Leu
                20

```

## (2) INFORMATION FOR SEQ ID NO:121:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

```

Ala Val Glu Ser Gly Met Leu Ala Leu Gly Thr Pro Ala Pro Ser
1           5           10           15

```

## (2) INFORMATION FOR SEQ ID NO:122:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

```

Ala Ala Met Lys Pro Arg Thr Gly Asp Gly Pro Leu Glu Ala Ala Lys
1           5           10           15

Glu Gly Arg

```

## (2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 15 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Tyr	Tyr	Trp	Cys	Pro	Gly	Gln	Pro	Phe	Asp	Pro	Ala	Trp	Gly	Pro
1				5					10					15

## (2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 14 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Asp	Ile	Gly	Ser	Glu	Ser	Thr	Glu	Asp	Gln	Gln	Xaa	Ala	Val
1				5					10				

## (2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 13 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Ala	Glu	Glu	Ser	Ile	Ser	Thr	Xaa	Glu	Xaa	Ile	Val	Pro
1				5					10			

## (2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 17 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Asp	Pro	Glu	Pro	Ala	Pro	Pro	Val	Pro	Thr	Thr	Ala	Ala	Ser	Pro	Pro
1				5					10					15	

Ser

## (2) INFORMATION FOR SEQ ID NO:127:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Ala Pro Lys Thr Tyr Xaa Glu Glu Leu Lys Gly Thr Asp Thr Gly  
 1                      5                      10                      15

## (2) INFORMATION FOR SEQ ID NO:128:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln Leu Thr Ser  
 1                      5                      10                      15

Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala Asn  
                     20                      25                      30

## (2) INFORMATION FOR SEQ ID NO:129:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Asp Pro Pro Asp Pro His Gln Xaa Asp Met Thr Lys Gly Tyr Tyr Pro  
 1                      5                      10                      15

Gly Gly Arg Arg Xaa Phe  
                     20

## (2) INFORMATION FOR SEQ ID NO:130:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Asp Pro Gly Tyr Thr Pro Gly  
 1                      5



## (2) INFORMATION FOR SEQ ID NO:131:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = Pro or Thr"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

```

Xaa Xaa Gly Phe Thr Gly Pro Gln Phe Tyr
1           5           10

```

## (2) INFORMATION FOR SEQ ID NO:132:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = Gln or Leu"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

```

Xaa Pro Xaa Val Thr Ala Tyr Ala Gly
1           5

```

## (2) INFORMATION FOR SEQ ID NO:133:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

```

Xaa Xaa Xaa Glu Lys Pro Phe Leu Arg
1           5

```

## (2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 15 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Xaa Asp Ser Glu Lys Ser Ala Thr Ile Lys Val Thr Asp Ala Ser  
 1                      5                      10                      15

## (2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 15 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Ala Gly Asp Thr Xaa Ile Tyr Ile Val Gly Asn Leu Thr Ala Asp  
 1                      5                      10                      15

## (2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 15 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Ala Pro Glu Ser Gly Ala Gly Leu Gly Gly Thr Val Gln Ala Gly  
 1                      5                      10                      15

## (2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Xaa Tyr Ile Ala Tyr Xaa Thr Thr Ala Gly Ile Val Pro Gly Lys Ile  
 1                      5                      10                      15

Asn Val His Leu Val  
 20

## (2) INFORMATION FOR SEQ ID NO:138:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 882 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

```

GCAACGCTGT CGTGGCCTTT GCGGTGATCG GTTTCGCCTC GCTGGCGGTG GCGGTGGCGG      60
TCACCATCCG ACCGACCGCG GCCTCAAAAC CGGTAGAGGG ACACCAAAAC GCCCAGCCAG      120
GGAAGTTCAT GCCGTTGTTG CCGACGCAAC AGCAGGCGCC GGTCCCGCCG CCTCCGCCCC      180
ATGATCCAC CGCTGGATTC CAGGGCGGCA CCATTCCGGC TGTACAGAAC GTGGTGCCGC      240
GGCCGGGTAC CTCACCCGGG GTGGGTGGGA CGCCGGCTTC GCCTGCGCCG GAAGCGCCGG      300
CCGTGCCCCG TGTGTGCCT GCCCGGTGC CAATCCCGGT CCCGATCATC ATCCCCCGT      360
TCCCGGGTTG GCAGCCTGGA ATGCCGACCA TCCCCACCGC ACCGCCGACG ACGCCGGTGA      420
CCACGTCGGC GACGACGCCG CCGACCACGC CGCCGACCAC GCCGGTGACC ACGCCGCCAA      480
CGACGCCGCC GACCACGCCG GTGACCACGC CGCCAACGAC GCCGCCGACC ACGCCGGTGA      540
CCACGCCACC AACGACCGTC GCCCCGACGA CCGTCGCCCC GACGACGGTC GCTCCGACCA      600
CCGTGCCCCG GACCACGGTC GCTCCAGCCA CCGCCACGCC GACGACCGTC GCTCCGCAGC      660
CGACGCAGCA GCCCAGCAA CAACCAACCC AACAGATGCC AACCCAGCAG CAGACCGTGG      720
CCCCGCAGAC GGTGGCGCCG GCTCCGCAGC CGCCGTCCGG TGGCCGCAAC GGCAGCGGCG      780
GGGGCGACTT ATTCGGCGGG TTCTGATCAC GGTGCGGGCT TCACTACGGT CGGAGGACAT      840
GGCCGGTGAT GCGGTGACGG TGGTGCTGCC CTGTCTCAAC GA                        882

```

## (2) INFORMATION FOR SEQ ID NO:139:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

```

CCATCAACCA ACCGCTCGCG CCGCCGCGC CGCCGGATCC GCCGTCGCCG CCACGCCCCG      60
CGGTGCCTCC GGTGCCCCCG TTGCCGCCGT CGCCGCCGTC GCCGCCGACC GGCTGGGTGC      120
CTAGGGCGCT GTTACCGCCC TGGTTGGCGG GGACGCCGCC GGCACCACCG GTACCGCCGA      180
TGGCGCCGTT GCCGCCGGCG GCACCGTTGC CACCGTTGCC ACCGTTGCCA CCGTTGCCGA      240
CCAGCCACCC GCCGCGACCA CCGGCACCGC CGGCGCCGCC CGCACCGCCG GCGTGCCCGT      300

```

TCGTGCCCCGT	ACCGCCGGCA	CCGCCGTTGC	CGCCGTCACC	GCCGACGGAA	CTACCGGCGG	360
ACGCGGCCTG	CCCGCCGGCG	CCGCCCAC	CGCCATTGGC	ACCGCCGTCA	CCGCCGGCTG	420
GGAGTGCCGC	GATTAGGGCA	CTGACCGGCG	CAACCAGCGC	AAGTACTCTC	GGTCACCGAG	480
CACTTCCAGA	CGACACCACA	GCACGGGGTT	GTCGGCGGAC	TGGGTGAAAT	GGCAGCCGAT	540
AGCGGCTAGC	TGTCGGCTGC	GGTCAACCTC	GATCATGATG	TCGAGGTGAC	CGTGACCGCG	600
CCCCCGAAG	GAGGCGCTGA	ACTCGGCGTT	GAGCCGATCG	GCGATCGGTT	GGGGCAGTGC	660
CCAGGCCAAT	ACGGGGATAC	CGGGTGTCNA	AGCCGCCGCG	AGCGCAGCTT	CGGTTGCGCG	720
ACNGTGGTCG	GGGTGGCCTG	TTACGCCGTT	GTCNTCGAAC	ACGAGTAGCA	GGTCTGCTCC	780
GGCGAGGGCA	TCCACCACGC	GTTGCGTCAG	CTCGT			815

## (2) INFORMATION FOR SEQ ID NO:140:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

ACCAGCCGCC	GGCTGAGGTC	TCAGATCAGA	GAGTCTCCGG	ACTCACCGGG	GCGGTTCAGC	60
CTTCTCCCAG	AACAACTGCT	GAAGATCCTC	GCCCCGAAA	CAGGCGCTGA	TTTGACGCTC	120
TATGACCGGT	TGAACGACGA	GATCATCCGG	CAGATTGATA	TGGCACCGCT	GGGCTAACAG	180
GTGCGCAAGA	TGGTGCAGCT	GTATGTCTCG	GACTCCGTGT	CGCGGATCAG	CTTTGCCGAC	240
GGCCGGGTGA	TCGTGTGGAG	CGAGGAGCTC	GGCGAGAGCC	AGTATCCGAT	CGAGACGCTG	300
GACGGCATCA	CGCTGTTTGG	GCGGCCGACG	ATGACAACGC	CCTTCATCGT	TGAGATGCTC	360
AAGCGTGAGC	GCGACATCCA	GCTCTTCACG	ACCGACGGCC	ACTACCAGGG	CCGGATCTCA	420
ACACCCGACG	TGTCATACGC	GCCGCGGCTC	CGTCAGCAAG	TTCACCGCAC	CGACGATCCT	480
GCGTTCTGCC	TGTCGTTAAG	CAAGCGGATC	GTGTCGAGGA	AGATCCTGAA	TCAGCAGGCC	540
TTGATTCGGG	CACACACGTC	GGGGCAAGAC	GTTGCTGAGA	GCATCCGCAC	GATGAAGCAC	600
TCGCTGGCCT	GGGTCGATCG	ATCGGGCTCC	CTGGCGGAGT	TGAACGGGTT	CGAGGGAAAT	660
GCCGCAAAGG	CATACTTCAC	CGCGCTGGGG	CATCTCGTCC	CGCAGGAGTT	CGCATTCCAG	720
GGCCGCTCGA	CTCGGCCGCC	GTTGGACGCC	TTCAACTCGA	TGGTCAGCCT	CGGCTATTCTG	780
CTGCTGTACA	AGAACATCAT	AGGGGCGATC	GAGCGTCACA	GCCTGAACGC	GTATATCGGT	840
TTCTTACACC	AGGATTCACG	AGGGCACGCA	ACGTCTCGTG	CCGAATTTCGG	CACGAGCTCC	900
GCTGAAACCG	CTGGCCGGCT	GCTCAGTGCC	CGTACGTAAT	CCGCTGCGCC	CAGGCCGGCC	960

CGCCGGCCGA ATACCAGCAG ATCGGACAGC GAATTGCCGC CCAGCCGGTT GGAGCCGTGC 1020  
 ATACCGCCGG CACACTCACC GGCAGCGAAC AGGCCTGGCA CCGTGGCGGC GCCGGTGTCC 1080  
 GCGTCTACTT CGACACCGCC CATCACGTAG TGACACGTCG GCCCGACTTC CATTGCCTGC 1140  
 GTTCGGCACG AG 1152

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 655 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

CTCGTGCCGA TTCGGCAGGG TGTACTTGCC GGTGGTGTAN GCCGCATGAG TGCCGACGAC 60  
 CAGCAATGCG GCAACAGCAC GGATCCCGGT CAACGACGCC ACCCGGTCCA CGTGGGCGAT 120  
 CCGCTCGAGT CCGCCCTGGG CGGCTCTTTC CTTGGGCAGG GTCATCCGAC GTGTTTCCGC 180  
 CGTGGTTTGC CGCCATTATG CCGGCGCGCC GCGTCGGGCG GCCGGTATGG CCGAANGTCG 240  
 ATCAGCACAC CCGAGATACG GGTCTGTGCA AGCTTTTTGA GCGTCGCGCG GGGCAGCTTC 300  
 GCCGGCAATT CTACTAGCGA GAAGTCTGGC CCGATACGGA TCTGACCGAA GTCGCTGCGG 360  
 TGCAGCCCAC CCTCATTGGC GATGGCGCCG ACGATGGCGC CTGGACCGAT CTTGTGCCGC 420  
 TTGCCGACGG CGACGCGGTA GGTGGTCAAG TCCGGTCTAC GCTTGGGCCT TTGCGGACGG 480  
 TCCCGACGCT GGTCGCGGTT GCGCCGCGAA AGCGGCGGGT CGGGTGCCAT CAGGAATGCC 540  
 TCACCGCCGC GGCAGTGCAC GGCCAGTGCC GCGGCGATGT CAGCCATCGG GACATCATGC 600  
 TCGCGTTCAT ACTCCTCGAC CAGTCGGCGG AACAGCTCGA TTCCCGGACC GCCCA 655

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 267 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Asn Ala Val Val Ala Phe Ala Val Ile Gly Phe Ala Ser Leu Ala Val  
 1 5 10 15  
 Ala Val Ala Val Thr Ile Arg Pro Thr Ala Ala Ser Lys Pro Val Glu  
 20 25 30  
 Gly His Gln Asn Ala Gln Pro Gly Lys Phe Met Pro Leu Leu Pro Thr  
 35 40 45

Gln Gln Gln Ala Pro Val Pro Pro Pro Pro Pro Asp Asp Pro Thr Ala  
 50 55 60  
 Gly Phe Gln Gly Gly Thr Ile Pro Ala Val Gln Asn Val Val Pro Arg  
 65 70 75 80  
 Pro Gly Thr Ser Pro Gly Val Gly Gly Thr Pro Ala Ser Pro Ala Pro  
 85 90 95  
 Glu Ala Pro Ala Val Pro Gly Val Val Pro Ala Pro Val Pro Ile Pro  
 100 105 110  
 Val Pro Ile Ile Ile Pro Pro Phe Pro Gly Trp Gln Pro Gly Met Pro  
 115 120 125  
 Thr Ile Pro Thr Ala Pro Pro Thr Thr Pro Val Thr Thr Ser Ala Thr  
 130 135 140  
 Thr Pro Pro Thr Thr Pro Pro Thr Thr Pro Val Thr Thr Pro Pro Thr  
 145 150 155 160  
 Thr Pro Pro Thr Thr Pro Val Thr Thr Pro Pro Thr Thr Pro Pro Thr  
 165 170 175  
 Thr Pro Val Thr Thr Pro Pro Thr Thr Val Ala Pro Thr Thr Val Ala  
 180 185 190  
 Pro Thr Thr Val Ala Pro Thr Thr Val Ala Pro Thr Thr Val Ala Pro  
 195 200 205  
 Ala Thr Ala Thr Pro Thr Thr Val Ala Pro Gln Pro Thr Gln Gln Pro  
 210 215 220  
 Thr Gln Gln Pro Thr Gln Gln Met Pro Thr Gln Gln Gln Thr Val Ala  
 225 230 235 240  
 Pro Gln Thr Val Ala Pro Ala Pro Gln Pro Pro Ser Gly Gly Arg Asn  
 245 250 255  
 Gly Ser Gly Gly Gly Asp Leu Phe Gly Gly Phe  
 260 265

## (2) INFORMATION FOR SEQ ID NO:143:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Ile Asn Gln Pro Leu Ala Pro Pro Ala Pro Pro Asp Pro Pro Ser Pro  
 1 5 10 15  
 Pro Arg Pro Pro Val Pro Pro Val Pro Pro Leu Pro Pro Ser Pro Pro  
 20 25 30  
 Ser Pro Pro Thr Gly Trp Val Pro Arg Ala Leu Leu Pro Pro Trp Leu  
 35 40 45

Ala Gly Thr Pro Pro Ala Pro Pro Val Pro Pro Met Ala Pro Leu Pro  
 50 55 60

Pro Ala Ala Pro Leu Pro Pro Leu Pro Pro Leu Pro Pro Leu Pro Thr  
 65 70 75 80

Ser His Pro Pro Arg Pro Pro Ala Pro Pro Ala Pro Pro Ala Pro Pro  
 85 90 95

Ala Cys Pro Phe Val Pro Val Pro Pro Ala Pro Pro Leu Pro Pro Ser  
 100 105 110

Pro Pro Thr Glu Leu Pro Ala Asp Ala Ala Cys Pro Pro Ala Pro Pro  
 115 120 125

Ala Pro Pro Leu Ala Pro Pro Ser Pro Pro Ala Gly Ser Ala Ala Ile  
 130 135 140

Arg Ala Leu Thr Gly Ala Thr Ser Ala Ser Thr Leu Gly His Arg Ala  
 145 150 155 160

Leu Pro Asp Asp Thr Thr Ala Arg Gly Cys Arg Arg Thr Gly  
 165 170

## (2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 35 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Gln Pro Pro Ala Glu Val Ser Asp Gln Arg Val Ser Gly Leu Thr Gly  
 1 5 10 15

Ala Val Gln Pro Ser Pro Arg Thr Thr Ala Glu Asp Pro Arg Pro Arg  
 20 25 30

Asn Arg Arg  
 35

## (2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 104 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Arg Ala Asp Ser Ala Gly Cys Thr Cys Arg Trp Cys Xaa Pro His Glu  
 1 5 10 15

Cys Arg Arg Pro Ala Met Arg Gln Gln His Gly Ser Arg Ser Thr Thr  
 20 25 30

Pro Pro Gly Pro Arg Gly Arg Ser Ala Arg Val Arg Pro Gly Arg Leu  
           35                          40                          45  
 Phe Pro Trp Ala Gly Ser Ser Asp Val Phe Pro Pro Trp Phe Ala Ala  
       50                                  55                          60  
 Ile Met Pro Ala Arg Arg Val Gly Arg Pro Val Trp Pro Xaa Val Asp  
   65                          70                          75                          80  
 Gln His Thr Arg Asp Thr Gly Leu Cys Lys Leu Phe Glu Arg Arg Ala  
                           85                          90                          95  
 Gly Gln Leu Arg Arg Gln Phe Tyr  
                           100

## (2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 53 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GGATCCATAT GGGCCATCAT CATCATCATC ACGTGATCGA CATCATCGGG ACC

53

## (2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 42 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

CCTGAATTCA GGCCTCGGTT GCGCCGGCCT CATCTTGAAC GA

42

## (2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

GGATCCTGCA GGCTCGAAAC CACCGAGCGG T

31



## (2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

CTCTGAATTC AGCGCTGGAA ATCGTCGCGA T 31

## (2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GGATCCAGCG CTGAGATGAA GACCGATGCC GCT 33

## (2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GAGAGAATTC TCAGAAGCCC ATTTGCGAGG ACA 33

## (2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1993 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 152..1276

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

TGTTCTTCGA CGGCAGGCTG GTGGAGGAAG GGCCACCGA ACAGCTGTTC TCCTCGCCGA 60

AGCATGCGGA AACCGCCCGA TACGTCGCCG GACTGTCTGGG GGACGTCAAG GACGCCAAGC 120

GCGGAAATTG AAGAGCACAG AAAGGTATGG C GTG AAA ATT CGT TTG CAT ACG 172

Val Lys Ile Arg Leu His Thr

1

5

CTG	TTG	GCC	GTG	TTG	ACC	GCT	GCG	CCG	CTG	CTG	CTA	GCA	GCG	GCG	GCG	220
Leu	Leu	Ala	Val	Leu	Thr	Ala	Ala	Pro	Leu	Leu	Leu	Ala	Ala	Ala	Gly	
		10					15					20				
TGT	GGC	TCG	AAA	CCA	CCG	AGC	GGT	TCG	CCT	GAA	ACG	GGC	GCC	GGC	GCC	268
Cys	Gly	Ser	Lys	Pro	Pro	Ser	Gly	Ser	Pro	Glu	Thr	Gly	Ala	Gly	Ala	
	25					30					35					
GGT	ACT	GTC	GCG	ACT	ACC	CCC	GCG	TCG	TCG	CCG	GTG	ACG	TTG	GCG	GAG	316
Gly	Thr	Val	Ala	Thr	Thr	Pro	Ala	Ser	Ser	Pro	Val	Thr	Leu	Ala	Glu	
40					45					50					55	
ACC	GGT	AGC	ACG	CTG	CTC	TAC	CCG	CTG	TTC	AAC	CTG	TGG	GGT	CCG	GCC	364
Thr	Gly	Ser	Thr	Leu	Leu	Tyr	Pro	Leu	Phe	Asn	Leu	Trp	Gly	Pro	Ala	
				60					65					70		
TTT	CAC	GAG	AGG	TAT	CCG	AAC	GTC	ACG	ATC	ACC	GCT	CAG	GGC	ACC	GGT	412
Phe	His	Glu	Arg	Tyr	Pro	Asn	Val	Thr	Ile	Thr	Ala	Gln	Gly	Thr	Gly	
			75					80					85			
TCT	GGT	GCC	GGG	ATC	GCG	CAG	GCC	GCC	GCC	GGG	ACG	GTC	AAC	ATT	GGG	460
Ser	Gly	Ala	Gly	Ile	Ala	Gln	Ala	Ala	Ala	Gly	Thr	Val	Asn	Ile	Gly	
		90					95					100				
GCC	TCC	GAC	GCC	TAT	CTG	TCG	GAA	GGT	GAT	ATG	GCC	GCG	CAC	AAG	GGG	508
Ala	Ser	Asp	Ala	Tyr	Leu	Ser	Glu	Gly	Asp	Met	Ala	Ala	His	Lys	Gly	
	105					110					115					
CTG	ATG	AAC	ATC	GCG	CTA	GCC	ATC	TCC	GCT	CAG	CAG	GTC	AAC	TAC	AAC	556
Leu	Met	Asn	Ile	Ala	Leu	Ala	Ile	Ser	Ala	Gln	Gln	Val	Asn	Tyr	Asn	
120					125					130					135	
CTG	CCC	GGA	GTG	AGC	GAG	CAC	CTC	AAG	CTG	AAC	GGA	AAA	GTC	CTG	GCG	604
Leu	Pro	Gly	Val	Ser	Glu	His	Leu	Lys	Leu	Asn	Gly	Lys	Val	Leu	Ala	
				140					145					150		
GCC	ATG	TAC	CAG	GGC	ACC	ATC	AAA	ACC	TGG	GAC	GAC	CCG	CAG	ATC	GCT	652
Ala	Met	Tyr	Gln	Gly	Thr	Ile	Lys	Thr	Trp	Asp	Asp	Pro	Gln	Ile	Ala	
			155					160					165			
GCG	CTC	AAC	CCC	GGC	GTG	AAC	CTG	CCC	GGC	ACC	GCG	GTA	GTT	CCG	CTG	700
Ala	Leu	Asn	Pro	Gly	Val	Asn	Leu	Pro	Gly	Thr	Ala	Val	Val	Pro	Leu	
		170					175					180				
CAC	CGC	TCC	GAC	GGG	TCC	GGT	GAC	ACC	TTC	TTG	TTC	ACC	CAG	TAC	CTG	748
His	Arg	Ser	Asp	Gly	Ser	Gly	Asp	Thr	Phe	Leu	Phe	Thr	Gln	Tyr	Leu	
	185					190					195					
TCC	AAG	CAA	GAT	CCC	GAG	GGC	TGG	GGC	AAG	TCG	CCC	GGC	TTC	GGC	ACC	796
Ser	Lys	Gln	Asp	Pro	Glu	Gly	Trp	Gly	Lys	Ser	Pro	Gly	Phe	Gly	Thr	
200					205					210					215	
ACC	GTC	GAC	TTC	CCG	GCG	GTG	CCG	GGT	GCG	CTG	GGT	GAG	AAC	GGC	AAC	844
Thr	Val	Asp	Phe	Pro	Ala	Val	Pro	Gly	Ala	Leu	Gly	Glu	Asn	Gly	Asn	
				220					225					230		
GGC	GGC	ATG	GTG	ACC	GGT	TGC	GCC	GAG	ACA	CCG	GGC	TGC	GTG	GCC	TAT	892
Gly	Gly	Met	Val	Thr	Gly	Cys	Ala	Glu	Thr	Pro	Gly	Cys	Val	Ala	Tyr	
			235					240					245			

ATC GGC ATC AGC TTC CTC GAC CAG GCC AGT CAA CGG GGA CTC GGC GAG Ile Gly Ile Ser Phe Leu Asp Gln Ala Ser Gln Arg Gly Leu Gly Glu 250 255 260	940
GCC CAA CTA GGC AAT AGC TCT GGC AAT TTC TTG TTG CCC GAC GCG CAA Ala Gln Leu Gly Asn Ser Ser Gly Asn Phe Leu Leu Pro Asp Ala Gln 265 270 275	988
AGC ATT CAG GCC GCG GCG GCT GGC TTC GCA TCG AAA ACC CCG GCG AAC Ser Ile Gln Ala Ala Ala Gly Phe Ala Ser Lys Thr Pro Ala Asn 280 285 290 295	1036
CAG GCG ATT TCG ATG ATC GAC GGG CCC GCC CCG GAC GGC TAC CCG ATC Gln Ala Ile Ser Met Ile Asp Gly Pro Ala Pro Asp Gly Tyr Pro Ile 300 305 310	1084
ATC AAC TAC GAG TAC GCC ATC GTC AAC AAC CGG CAA AAG GAC GCC GCC Ile Asn Tyr Glu Tyr Ala Ile Val Asn Asn Arg Gln Lys Asp Ala Ala 315 320 325	1132
ACC GCG CAG ACC TTG CAG GCA TTT CTG CAC TGG GCG ATC ACC GAC GGC Thr Ala Gln Thr Leu Gln Ala Phe Leu His Trp Ala Ile Thr Asp Gly 330 335 340	1180
AAC AAG GCC TCG TTC CTC GAC CAG GTT CAT TTC CAG CCG CTG CCG CCC Asn Lys Ala Ser Phe Leu Asp Gln Val His Phe Gln Pro Leu Pro Pro 345 350 355	1228
GCG GTG GTG AAG TTG TCT GAC GCG TTG ATC GCG ACG ATT TCC AGC Ala Val Val Lys Leu Ser Asp Ala Leu Ile Ala Thr Ile Ser Ser 360 365 370	1273
TAGCCTCGTT GACCACCACG CGACAGCAAC CTCCGTCGGG CCATCGGGCT GCTTTGCGGA	1333
GCATGCTGGC CCGTGCCGGT GAAGTCGGCC GCGCTGGCCC GGCCATCCGG TGGTTGGGTG	1393
GGATAGGTGC GGTGATCCCG CTGCTTGCGC TGGTCTTGGT GCTGGTGGTG CTGGTCATCG	1453
AGGCGATGGG TGCGATCAGG CTCAACGGGT TGCATTTCTT CACCGCCACC GAATGGAATC	1513
CAGGCAACAC CTACGGCGAA ACCGTTGTCA CCGACGCGTC GCCCATCCGG TCGGCGCCTA	1573
CTACGGGGCG TTGCCGCTGA TCGTCGGGAC GCTGGCGACC TCGGCAATCG CCCTGATCAT	1633
CGCGGTGCCG GTCTCTGTAG GAGCGGCGCT GGTGATCGTG GAACGGCTGC CGAAACGGTT	1693
GGCCGAGGCT GTGGGAATAG TCCTGGAATT GCTCGCCGGA ATCCCCAGCG TGGTCGTCGG	1753
TTTGTGGGGG GCAATGACGT TCGGGCCGTT CATCGCTCAT CACATCGCTC CGGTGATCGC	1813
TCACAACGCT CCCGATGTGC CGGTGCTGAA CTAATTGCGC GGCGACCCGG GCAACGGGGA	1873
GGGCATGTTG GTGTCCGGTC TGGTGTTGGC GGTGATGGTC GTTCCCATTA TCGCCACCAC	1933
CACTCATGAC CTGTTCCGGC AGGTGCCGGT GTTGCCCCGG GAGGGCGCGA TCGGGAATTC	1993

## (2) INFORMATION FOR SEQ ID NO:153:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Val	Lys	Ile	Arg	Leu	His	Thr	Leu	Leu	Ala	Val	Leu	Thr	Ala	Ala	Pro	1	5	10	15
Leu	Leu	Leu	Ala	Ala	Ala	Gly	Cys	Gly	Ser	Lys	Pro	Pro	Ser	Gly	Ser	20	25	30	
Pro	Glu	Thr	Gly	Ala	Gly	Ala	Gly	Thr	Val	Ala	Thr	Thr	Pro	Ala	Ser	35	40	45	
Ser	Pro	Val	Thr	Leu	Ala	Glu	Thr	Gly	Ser	Thr	Leu	Leu	Tyr	Pro	Leu	50	55	60	
Phe	Asn	Leu	Trp	Gly	Pro	Ala	Phe	His	Glu	Arg	Tyr	Pro	Asn	Val	Thr	65	70	75	
Ile	Thr	Ala	Gln	Gly	Thr	Gly	Ser	Gly	Ala	Gly	Ile	Ala	Gln	Ala	Ala	85	90	95	
Ala	Gly	Thr	Val	Asn	Ile	Gly	Ala	Ser	Asp	Ala	Tyr	Leu	Ser	Glu	Gly	100	105	110	
Asp	Met	Ala	Ala	His	Lys	Gly	Leu	Met	Asn	Ile	Ala	Leu	Ala	Ile	Ser	115	120	125	
Ala	Gln	Gln	Val	Asn	Tyr	Asn	Leu	Pro	Gly	Val	Ser	Glu	His	Leu	Lys	130	135	140	
Leu	Asn	Gly	Lys	Val	Leu	Ala	Ala	Met	Tyr	Gln	Gly	Thr	Ile	Lys	Thr	145	150	155	
Trp	Asp	Asp	Pro	Gln	Ile	Ala	Ala	Leu	Asn	Pro	Gly	Val	Asn	Leu	Pro	165	170	175	
Gly	Thr	Ala	Val	Val	Pro	Leu	His	Arg	Ser	Asp	Gly	Ser	Gly	Asp	Thr	180	185	190	
Phe	Leu	Phe	Thr	Gln	Tyr	Leu	Ser	Lys	Gln	Asp	Pro	Glu	Gly	Trp	Gly	195	200	205	
Lys	Ser	Pro	Gly	Phe	Gly	Thr	Thr	Val	Asp	Phe	Pro	Ala	Val	Pro	Gly	210	215	220	
Ala	Leu	Gly	Glu	Asn	Gly	Asn	Gly	Gly	Met	Val	Thr	Gly	Cys	Ala	Glu	225	230	235	
Thr	Pro	Gly	Cys	Val	Ala	Tyr	Ile	Gly	Ile	Ser	Phe	Leu	Asp	Gln	Ala	245	250	255	
Ser	Gln	Arg	Gly	Leu	Gly	Glu	Ala	Gln	Leu	Gly	Asn	Ser	Ser	Gly	Asn	260	265	270	

Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Gly Phe  
 275 280 285  
 Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro  
 290 295 300  
 Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn  
 305 310 315 320  
 Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu  
 325 330 335  
 His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val  
 340 345 350  
 His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu  
 355 360 365  
 Ile Ala Thr Ile Ser Ser  
 370

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1993 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

TGTTCTTCGA CGGCAGGCTG GTGGAGGAAG GGCCACCGA ACAGCTGTTC TCCTCGCCGA	60
AGCATGCGGA AACCGCCCGA TACGTCGCCG GACTGTCTGGG GGACGTCAAG GACGCCAAGC	120
GCGGAAATTG AAGAGCACAG AAAGGTATGG CGTGAAAATT CGTTTGCATA CGCTGTTGGC	180
CGTGTTGACC GCTGCGCCGC TGCTGCTAGC AGCGGCGGGC TGTGGCTCGA AACCACCGAG	240
CGGTTCTGCCT GAAACGGGCG CCGGCGCCGG TACTGTCTCGG ACTACCCCGG CGTCGTCTGCC	300
GGTGACGTTG GCGGAGACCG GTAGCACGCT GCTCTACCCG CTGTTC AACC TGTGGGGTCC	360
GGCCTTTCAC GAGAGGTATC CGAACGTCAC GATCACCGCT CAGGGCACCG GTTCTGGTGC	420
CGGGATCGCG CAGGCCGCCG CCGGGACGGT CAACATTGGG GCCTCCGACG CCTATCTGTC	480
GGAAGGTGAT ATGGCCGCGC ACAAGGGGCT GATGAACATC GCGCTAGCCA TCTCCGCTCA	540
GCAGGTCAAC TACAACCTGC CCGGAGTGAG CGAGCACCTC AAGCTGAACG GAAAAGTCCT	600
GGCGGCCATG TACCAGGGCA CCATCAAAAC CTGGGACGAC CCGCAGATCG CTGCGCTCAA	660
CCCCGGCGTG AACCTGCCCC GCACCGCGGT AGTTCCGCTG CACCGCTCCG ACGGGTCCGG	720
TGACACCTTC TTGTTACCC AGTACCTGTC CAAGCAAGAT CCCGAGGGCT GGGGCAAGTC	780
GCCCCGCTTC GGCACCACCG TCGACTTCCC GGCGGTGCCG GGTGCGCTGG GTGAGAACGG	840
CAACGGCGGC ATGGTGACCG GTTGCGCCGA GACACCGGGC TCGGTGGCCT ATATCGGCAT	900

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CAGCTTCCTC GACCAGGCCA GTCAACGGGG ACTCGGCGAG GCCCAACTAG GCAATAGCTC      960
TGGCAATTTC TTGTTGCCCG ACGCGCAAAG CATTGAGGCC GCGGCGGCTG GCTTCGCATC      1020
GAAAACCCCG GCGAACCAGG CGATTTCGAT GATCGACGGG CCCGCCCCCG ACAGGCTACCC      1080
GATCATCAAC TACGAGTACG CCATCGTCAA CAACCGGCAA AAGGACGCCG CCACCGCGCA      1140
GACCTTGACG GCATTTCTGC ACTGGGCGAT CACCGACGGC AACAAAGGCCT CGTTCCTCGA      1200
CCAGGTTTCAT TTCCAGCCGC TGCCGCCCCG GGTGGTGAAG TTGTCTGACG CGTTGATCGC      1260
GACGATTTCC AGCTAGCCTC GTTGACCACC ACGCGACAGC AACCTCCGTC GGGCCATCGG      1320
GCTGCTTTGC GGAGCATGCT GGCCCGTGCC GGTGAAGTCG GCCGCGCTGG CCCGGCCATC      1380
CGGTGGTTGG GTGGGATAGG TGCGGTGATC CCGCTGCTTG CGCTGGTCTT GGTGCTGGTG      1440
GTGCTGGTCA TCGAGGCGAT GGGTGCGATC AGGCTCAACG GGTGTCATTT CTTACCGCC      1500
ACCGAATGGA ATCCAGGCAA CACCTACGGC GAAACCGTTG TCACCGACGC GTCGCCCATC      1560
CGGTGCGCGC CTACTACGGG GCGTTGCCGC TGATCGTCGG GACGCTGGCG ACCTCGGCAA      1620
TCGCCCTGAT CATCGCGGTG CCGGTCTCTG TAGGAGCGGC GCTGGTGATC GTGGAACGGC      1680
TGCCGAAACG GTTGGCCGAG GCTGTGGGAA TAGTCCTGGA ATTGCTCGCC GGAATCCCCA      1740
GCGTGGTCGT CGGTTTGTGG GGGGCAATGA CGTTCGGGCC GTTCATCGCT CATCACATCG      1800
CTCCGGTGAT CGCTCACAAC GCTCCCGATG TGCCGGTGCT GAACTACTTG CGCGGCGACC      1860
CGGGCAACGG GGAGGGCATG TTGGTGTCCG GTCTGGTGTT GCGGTGATG GTCGTTCCCA      1920
TTATCGCCAC CACCACTCAT GACCTGTTCC GGCAGGTGCC GGTGTTGCCC CGGGAGGGCG      1980
CGATCGGGAA TTC                                                                1993

```

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

```

Met Lys Ile Arg Leu His Thr Leu Leu Ala Val Leu Thr Ala Ala Pro
1           5           10           15

Leu Leu Leu Ala Ala Ala Gly Cys Gly Ser Lys Pro Pro Ser Gly Ser
          20           25           30

Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
          35           40           45

Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
          50           55           60

```

Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr  
 65 70 75 80  
 Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala  
 85 90 95  
 Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly  
 100 105 110  
 Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser  
 115 120 125  
 Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys  
 130 135 140  
 Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr  
 145 150 155 160  
 Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro  
 165 170 175  
 Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr  
 180 185 190  
 Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly  
 195 200 205  
 Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly  
 210 215 220  
 Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu  
 225 230 235 240  
 Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala  
 245 250 255  
 Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn  
 260 265 270  
 Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Gly Phe  
 275 280 285  
 Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro  
 290 295 300  
 Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn  
 305 310 315 320  
 Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu  
 325 330 335  
 His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val  
 340 345 350  
 His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu  
 355 360 365  
 Ile Ala Thr Ile Ser Ser  
 370